

31

[illegible]

KEYWORDS	SOURCE	ORGANISM
Homo sapiens.	Homo sapiens	

TITLE	AUTHORS
Cloning and characterization of the cDNA and gene for human $\alpha_2(\text{M})$ microglobulin	Uccignelli, E., Rao, N. V., Rao, G. V., Zhengming, W., Alberline, K. H. and Hoidal, J. R.

TITLE Hoidal, J.R.
DIRECT SUBMISSION Direct Submission
SUBMITTED (15-DEC-2000) Pulmonary Medicine, University of Utah,
JOURNAL

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/chromosome="21"
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/gene="TMPRSS2"
/note="protease; PRSS10"
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908 908 710 4

BASE 1 CONTINUED

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Matches 3188; Conservative	0	Mismatches 8	Indels 6; Gaps 5

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Db	61	GAGCGCGCAGGCTCATATTTGAACATTTCCACATACATATGACTGATGATGCTGTGATTA	120
OY	142	CAGCAAGATGGCTTTGAAGTACAGGGTACACCAGCTATTGGACCTTACTATGAAACCA	201
Db	121	CAGCAAGATGGCTTTGAAGTACAGGGTACACCAGCTATTGGACCTTACTATGAAACCA	180
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QY	1822	CTAACCCCTTGTCCGCAAGGGGTGATGGCGCTGTGGTATGGGCACTGAGCGTCAAGTGT	1881
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QY	1882	GGAGAGAGGGGTGAGAGGCTGCCCCAATTAGATCTTCTGCTGAGTCCCTTTCAGAGGGCC	1941
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QY	1942	AATTTTGGATGAGATGAGGACTGTCACCTCTCAGCTGCTGAGTGAATGACTTGAATGAAAAG	2001
Db	1920	AATTTTGGATGAGATGAGGACTGTCACCTCTCAGCTGCTGAGTGAATGACTTGAATGAAAAG	1979
QY	2002	GAGAGACATGAAAAGGAGACAGCCACAGGTGGCACCTGCAGAGCGCGTGC - CTTGAGGGCCAC	2060
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Qy	2361	CTCCCTGACCCCTGGTCCCTAGACCCCTGGAGAGTGCACATGCCCCCTTGGTCTCGGGGACGG	2420
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Qy	2661	CTTTGACAAAATGACTGGCTCTGACTTAAAGTTCTATATAATGATGTGCTGAAAGCAAG	2720
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Qy	2781	TTCCAACTGCTGTGGGTTTCCAAACGAGGGAAGGCTCCCTTTGCAATGCGCAAGTCCATA	2840
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Db	3056	GAAAGAGTCTCTCTTTTTCGCCCTCTTATTTATGTGAAACACTGTTGTCTTTTT	3115
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AX201121			

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 08:38:25 ; Search time 631 Seconds
(without alignments)
12287.845 Million cell updates/sec

Title: US-09-807-201-8
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3441.4	100.0	3443	AA295005	Cancer specific ge
2	3331.8	96.8	3483	ABV21748	Human prostate exp
3	3331.8	96.8	3483	ABV21767	Human prostate exp
4	3331.8	96.8	3483	ABV21318	Human prostate exp
5	3331.8	96.8	3483	ABV27570	Human prostate exp
6	3331.8	96.8	3483	ABV27589	Human prostate exp
7	3331.8	96.8	3483	ABV29119	Human prostate exp
8	3330.2	96.7	3483	ABV24651	Human prostate exp
9	3330.2	96.7	3483	ABV29165	Human prostate exp

10	3236.6	94.0	3966	21	AAC83325	Human TMPRSS2 DNA.
11	3136.8	91.1	3245	21	AAA08803	Androgen-inducible
12	3136.8	91.1	3245	22	AA564178	Human prostate cDN
13	3136.8	91.1	3245	22	AAH93942	P1000C full length
14	3136.8	91.1	3245	24	ABL95549	Human P1000C cDNA
15	2309.4	67.1	2479	21	AAZ90478	Ovrl15 homolog pro
16	2309.4	67.1	2479	21	AAZ87813	Human tumour supp
17	2309.4	67.1	2479	22	AA564164	Human CDNA encodin
18	2309.4	67.1	2479	22	AAAD13168	Human serine prote
19	2309.4	67.1	2479	22	AAH93928	Human transmembran
20	2309.4	67.1	2479	24	ABK92201	Prostate cancer-as
21	2309.4	67.1	2479	24	ABJ95535	Human transmembran
22	2309.4	67.1	2479	24	AAZ28779	Human TMPRSS2 gene
23	1710.4	49.7	1738	21	AAZ29636	Human 20P1F12-GTC2
24	1710.4	49.7	1738	21	AAZ28778	Human 20P1F12-GTC1
25	1464.8	42.5	1479	22	AA564179	Human tumour supp
26	1464.8	42.5	1479	22	AAH93943	Human prostate cDN
27	1464.8	42.5	1479	24	ABJ95550	Human P1000C cDNA
28	1464.8	42.5	1476	22	AA564180	Human prostate cDN
29	1461.8	42.5	1476	22	AAH93944	P1000C open readin
30	1461.8	42.5	1476	24	ABL95551	Human P1000C cDNA
31	1461.8	42.5	1476	24	AAA12975	CDNA encoding huma
32	983	28.6	1076	21	AAZ27930	Human prostate-ass
33	983	28.6	1077	24	AAZ27930	Human prostate-ass
34	862.6	25.1	2172	21	AAZ27930	Human prostate-ass
35	681.4	19.8	683	22	AA564165	Human CDNA encodin
36	681.4	19.8	683	22	AAH93929	Human transmembran
37	681.4	19.8	683	24	ABL95536	Human transmembran
38	592	17.2	670	23	ABV44257	Human prostate exp
39	592	17.2	670	23	ABV44318	Human prostate exp
40	490	14.2	557	21	AAA06603	Human immunogenic
41	490	14.2	557	22	AA563812	Human prostate cDN
42	490	14.2	557	22	AAH93719	Human prostate-spe
43	490	14.2	557	22	AAH85033	Human prostate-spe
44	490	14.2	557	22	AAH02784	Prostate tumour an
45	490	14.2	557	24	ABL95183	Human P1000C cDNA

ALIGNMENTS

RESULT 1						
AA295005						
ID	AA295005	standard;	CDNA;	3443	BP.	
XX						
AC	AA295005;					
XX						
DT	15-AUG-2000	(first entry)				
XX						
DE	Cancer specific gene Prol15 useful as prostate cancer marker.					
XX						
KW	Prostate cancer; cancer specific gene; CSG; diagnosis; monitoring; staging; imaging; therapy; metastasis; marker; human; Prol15; ds.					
XX						
OS	Homo sapiens.					
XX						
PN	WO200023111-A1.					
XX						
PD	27-APR-2000.					
XX						
PF	19-OCT-1999;	99WO-US24331.				
XX						
PR	19-OCT-1998;	98US-0104737.				
XX						
PA	(DIAD-) DIADEXUS LLC.					
XX						
PI	Salceda S, Reipon H, Cafferkey R;					
XX						
DR	WPI; 2000-339531/29.					
XX						
PT	Diagnosing, staging and monitoring the presence and metastases of prostate cancer especially useful for treating prostate cancer					
PT	comprises measuring changes in cancer specific gene levels -					

XX Claim 7, page 57-58, 74pp; English.
 XX The present sequence is that of a full-length contig for cancer
 CC specific gene (CSG) Prolis (clone 2189835H): a corresponding
 CC expressed sequence tag is given in AA295004. The CSG was identified
 CC in a database search using the data mining Cancer Leads Automatic
 CC Search Package (CLASP), which allows the identification of highly
 CC expressed organ and cancer specific genes. Overexpression of
 CC Prolis was observed in 3 of 4 primary prostate cancer tissues
 CC examined, indicative of it being a diagnostic marker for prostate
 CC cancer. The invention provides ESTs and full-length contigs for
 CC prostate CSGs (see AA24998-295017). The CSGs, polypeptides encoded
 CC by them, and antibodies that specifically bind CSG are used in new,
 CC claimed methods for detecting, diagnosing, monitoring, staging,
 CC imaging and treating prostate cancer. The new methods provide
 CC earlier diagnosis for the presence and metastasis of prostate
 CC cancer, and can be used to determine if a cancer has metastasized,
 CC or to monitor the progress or stage of the disease when it has not
 CC metastasized.
 CC
 XX
 SQ Sequence 3443 BP; 793 A; 866 C; 938 G; 846 T; 0 other;

Query Match 100.0%; Score 3441.4; DB 21; Length 3443;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 1 GGGCGGGCCGGCCGAGTAGCGGAGCTAAGCAGAGGCGGAGGCGGAGGCGG 60
 YY 61 AGGGGGGGGAGCCCGCTGGAGCGGCGGAGTATATGACATTCAGATACCTATC 120
 DB 61 AGGGGGGGGAGCCCGCTGGAGCGGCGGAGTATATGACATTCAGATACCTATC 120
 YY 121 ATTACTGATCTGTGTATACAGCAAGATGGCTTGAACACAGGCTACCAACGCTAT 180
 DB 121 ATTACTGATCTGTGTATACAGCAAGATGGCTTGAACACAGGCTACCAACGCTAT 180
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 DB 421 GGGGACCTTCTCTGTGGAGCTGCGCTGGCCGCTGCTACTCTGGAAGTTGATGGCAG 480
 YY 481 CAATGTCTCCAACTCTGGGATAGAGTGGAGTCTCTGAGTACCTGATCAACCCCTCTAA 540
 DB 481 CAATGTCTCCAACTCTGGGATAGAGTGGAGTCTCTGAGTACCTGATCAACCCCTCTAA 540
 YY 541 CTGCTGTGATGGCTGTACACTGCCCGGGGGGAGAGAGATGGGTGTGGCT 600
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 YY 601 CTACGAGCAAACTTCATCTTCAAGGTGTACTCATCTCAGAGAACTCTGGCAACCTGT 660
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 RESULT 2
 ABY21748
 ID ABY21748 standard; cDNA; 3483 BP.
 AC ABY21748;
 DT 13-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 21739.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 PN W0200160860-A2.
 PD 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US05171.
 PF
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
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 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JR;
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 Db 3427 GCTGTCTCTGTGTGAGAGTGTGCTCAATGATCTCTTATTTATTTATTTAGTCTG 3483
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 ID ABV21767 standard; cDNA; 3483 BP.
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 AC ABV21767;
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 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21758.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KM pharmacogenomic marker; gene: ss.
 OS Homo sapiens.
 PN
 WO200160860-A2.
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.


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Db 3427 GCTGTCTCTGTTGAGAGAGTCCCTCAATGATCTCTTATTTATTTATTTAGTCTG 3483

RESULT 4
ABV23318
ID ABV23318 standard; cDNA; 3483 BP.
XX
AC ABV23318;
XX
DE Human prostate expression marker cDNA 23309.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PE 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
XX 16-MAR-2000; 2000US-189862P.
XX 15-MAY-2000; 2000US-207454P.
XX 09-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX

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Db	1872	GCCGTCTCTCCCTAACCCCTTGTGTGCGCAAGGGGTGATGGCCGGTGTGTGTGGGCATGG	1931
Qy	1871	CGGTCAAGTCTGGAGGAGAGAGGGGTGGAGGGCTGCCCATTTGATCTCTCTGTAGTCTCT	1930
Db	1932	CGGTCAAGTCTGGAGGAGAGGGGTGGAGGGCTGCCCATTTGATCTCTCTGTAGTCTCT	1991
Qy	1931	TTTCCAGGGGGCAATTTTGGATGTAGCATGTGAGCTGTACCTCTCACCTCTGTGGATCTTG	1990
Db	1992	TTTCCAGGGGGCAATTTTGGATGTAGCATGTGAGCTGTACCTCTCACCTCTGTGGATCTTG	2051
Qy	2050	TTCTGGGGCCACTTGTGTAGTGTCTCCCAAGCTTACCTCTCCCAAGGGGATTTTGTGTATGG	2109
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Qy	2110	TTTCTTAGAGCTTTAGCAGCCCTGGATGTGGCGAGAAATTAAGGGAGACAGCCCTTACATGG	2169
Db	2172	TTTCTTAGAGCTTTAGCAGCCCTGGATGTGGCGAGAAATTAAGGGAGACAGCCCTTACATGG	2231
Qy	2170	GTGTGTGACGTGTAGTACCTCTTAAAGGGGAAACAGAAATTTTGTCTTATAGGGGTGA	2229
Db	2232	GTGTGTGACGTGTAGTACCTCTTAAAGGGGAAACAGAAATTTTGTCTTATAGGGGTGA	2290
Qy	2230	GAAATATGACATGTCCCTTGTGGTGGCGAGGAAAGCAATTTGAAGAAGACTTGTCCCTGAGCA	2289
Db	2291	GAAATATGACATGTCCCTTGTGGTGGCGAGGAAAGCAATTTGAAGAAGACTTGTCCCTGAGCA	2349
Qy	2290	CTCTGTGTGAGGAGTCTCCACATCTGACATTTGGGGGGCTCCGGAGGGAGAGTCAAGCT	2349
Db	2350	CTCTGTGTGAGGAGTCTCCACATCTGACATTTGGGGGGCTCCGGAGGGAGAGTCAAGCT	2409
Qy	2350	TTCTCTCATCTCTCCCTGACACCTGTCTCTAGACACCTTGAGAGTGTACATGTGCCCTTGGT	2409
Db	2410	TTCTCTCATCTCTCCCTGACACCTGTCTCTAGACACCTTGAGAGTGTACATGTGCCCTTGGT	2469
Qy	2410	CTGTGGGAGGGGGCCCAAGTCTGGACCAATGTGGCTTTCAGGCTCTGTAGTCACTGG	2469
Db	2470	CTGTGGGAGGGGGCCCAAGTCTGGACCAATGTGGCTTTCAGGCTCTGTAGTCACTGG	2527
Qy	2470	AAATTTGAGTGTCCATGGGGGAAATCAAGAGTGTCTCAAGTTAAGTTCACATGTTCATATTT	2529
Db	2528	AAATTTGAGTGTCCATGGGGGAAATCAAGAGTGTGTCTCAAGTTAAGTTCACATGTTCATATTT	2587
Qy	2530	ATGTCTTCTACACATTTGCTTACCTCAGTACGTCTGTGGAAGTCTTACTTTTANTGTCTCCACAT	2589
Db	2588	ATGTCTTCTACACATTTGCTTACCTCAGTACGTCTGTGGAAGTCTTACTTTTANTGTCTCCACAT	2647
Qy	2590	AGTCCACCTTCATTTAACTCTTTGAAACGTATCATCTTTGCCAAGTAAAGTGTGTGCC	2649
Db	2648	AGTCCACCTTCATTTAACTCTTTGAAACGTATCATCTTTGCCAAGTAAAGTGTGTGCC	2707
Qy	2650	TATTTTACAGCTCTTTTGACAAAATGACTGGCTCTGTACTTAATGATGATGTG	2709
Db	2708	TATTTTACAGCTCTTTTGACAAAATGACTGGCTCTGTACTTAATGATGATGTG	2767
Qy	2710	CTGAAGCAAAAGTGCCTTGTGGTGGCGCGAGAAAGAAAGATGTCTTTTGTGTTTGGATCTG	2769
Db	2768	CTGAAGCAAAAGTGCCTTGTGGTGGCGCGAGAAAGAAAGATGTCTTTTGTGTTTGGATCTG	2827
Qy	2770	TTCTGTGCTTCTTCCATGTCTGTGGGTTCACACAGGGGAAAGGGTCCCTTTTGATCTGC	2829
Db	2828	TTCTGTGCTTCTTCCATGTCTGTGGGTTCACACAGGGGAAAGGGTCCCTTTTGATCTGC	2887
Qy	2830	CAAGTGCATTAACCATGAGACATCACTCTACATGGTTTGTCTCTCTGTGGCAAGAGCTGTG	2889
Db	2888	CAAGTGCATTAACCATGAGACATCACTCTACATGGTTTGTCTCTCTGTGGCAAGAGCTGTG	2947

QY	2890	GTTCAGAAATGAATGAATGATTCCTACGTAGAGACTAATCCTTGAATGAAAGTCT	2949
Db	2948	TTTTCCAAAGAAATGAATGATGATTCCTACGTAGAGACTAATCCTTGAATGAAAGTCT	3007
QY	2950	TGCATATCCCATTTGGACAGATCCGCTGTGTGCACATGCGCTGTGTAGAGAGACATTTCCAG	3009
.Db	3008	TGCATATCCCATTTGGACAGATCCGCTGTGTGCACATGCGCTGTGTAGAGAGACATTTCCAG	3067
QY	3010	GGACCTTGGAAACAGTTGGCACTGTAAAGTGTCTGCTCCCAAGACACATCCTAAAAAGT	3069
Db	3068	GGACCTTGGAAACAGTTGGCACTGTAAAGTGTCTGCTCCCAAGACACATCCTAAAAAGT	3127
QY	3070	GTTGTAATGGTAAAAACGCTTCCTCTTATTTGGCCCTCTTATTTATGTAACAATCG	3129
Db	3128	TTTTTAATGGTAAAAACGCTTCCTCTTATTTGGCCCTCTTATTTATGTAACAATCG	3187
QY	3130	TTTTCTTTTCTTTTGTATCTTTTAAACGTAAAGTTCAATGTGAAATGAATATCATG	3189
Db	3188	TTTTCTTTTCTTTTGTATCTTTTAAACGTAAAGTTCAATGTGAAATGAATATCATG	3247
QY	3190	CAATTAATTTATGCGATTTTCTTCAAAAGTAAACACATCATCTTTGAAAGTCTGCTGG	3249
Db	3248	CAATTAATTTATGCGATTTTCTTCAAAAGTAAACACATCATCTTTGAAAGTCTGCTGG	3307
QY	3250	TGAGTAGAGACACGCTCCATTTCCCTATTAAGGGGGGATGTAGAGCTGCTGTAGAGG	3309
Db	3308	TGAGTAGAGACACGCTCCATTTCCCTATTAAGGGGGGATGTAGAGCTGCTGTAGAGG	3367
QY	3310	ACCAAGGTGAGGACAGGCGACAGCTGTGTCTCTGTGGTGGCGCCACAGTCTGTGA	3369
Db	3368	ACCAAGGTGAGGACAGGCGGACCTGTGTGTGTGTGTGGTGGCGCCACAGTCTGTGA	3426
QY	3370	GCCTGTCTCTGTGTGAGAGGTCCTCAATGACTCCTTCTTATTTATTAAGCTCG	3426
Db	3427	GCCTGTCTCTGTGTGAGAGGTCCTCAATGACTCCTTCTTATTTATTAAGCTCG	3483
RESULT 5			
ABV27570	ID	ABV27570 standard; cDNA; 3483 BP.	
XX	XX	ABV27570;	
AC	AC	ABV27570;	
XX	XX	16-SEP-2002 (first entry)	
DT	DT	16-SEP-2002 (first entry)	
XX	XX	Human prostate expression marker cDNA 27561.	
DE	DE	Human prostate expression marker cDNA 27561.	
XX	XX	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;	
KW	KW	pharmacogenomic marker; gene; ss.	
XX	XX	Homo sapiens.	
OS	OS	Homo sapiens.	
XX	PN	WO200160860-A2.	
XX	XX	23-AUG-2001.	
PD	PD	23-AUG-2001.	
XX	XX	20-FEB-2001; 2001WO-US05171.	
PF	PF	17-FEB-2000; 2000US-183319P.	
PR	PR	16-MAR-2000; 2000US-189862P.	
PR	PR	25-MAY-2000; 2000US-207454P.	
PR	PR	09-JUN-2000; 2000US-211314P.	
PR	PR	18-JUL-2000; 2000US-219007P.	
PR	PR	13-DEC-2000; 2000US-255281P.	
XX	XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
PA	PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX	XX	Schlegel R, Endege WO, Monahan JE;	
PI	PI	Schlegel R, Endege WO, Monahan JE;	
XX	XX	WPI; 2001-662795/76.	
DR	DR	Novel isolated nucleic acid molecule associated with cancerous state of	

1811 GCCTGCTCCTTAACCCCTTGTCCGAAGGGGTGATGCGCGGTGTTGTGGGCACTGG 1870
1872 GCCTGCTCCTTAACCCCTTGTCCGAAGGGGTGATGCGCGGTGTTGTGGGCACTGG 1931
1871 CGGTCAAGTGTGGAGAGAGGGGGTGGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCT 1930
1932 CGGTCAAGTGTGGAGAGAGGGGGTGGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCT 1991
1931 TTTCAGAGGGGCCAATTTTGTGATGAGCATGAGCTGTACCTCTCAGCTGCTGATGACTTG 1990
1992 TTTCAGAGGGGCCAATTTTGTGATGAGCATGAGCTGTACCTCTCAGCTGCTGATGACTTG 2051
1991 AGATCAAAAAGAGAGACATGGAAGAGAGACAGCCAGTGGCAGCTGAGCGGCTG-CC 2049
2052 AGATCAAAAAGAGAGACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2111
2050 TCTGGGGCAGCTGTGATGAGTGTCCAGCTTCTCCCAAGGGGATTTTCTGATGGG 2109
2112 TCTGGGGCAGCTGTGATGAGTGTCCAGCTTCTCCCAAGGGGATTTTCTGATGGG 2171
2110 TTCTTAGAGCCCTTACAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATG 2169
2172 TTCTTAGAGCCCTTACAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATG 2231
2170 GTGTGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2229
2232 GTGTGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2290
2230 GAATTAACAGAGTGGCTTGGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2289
2291 GAATTAACAGAGTGGCTTGGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2349
2290 CTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2349
2350 CTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2409
2350 TCTCTCTCATCT 2409
2410 TCTCTCTCATCT 2469
2410 CCTGGGAGGGGGGCGGAGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2469
2470 CCTGG--CAGGGGCGCAAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2527
2470 AAATTGAGTCCATGGGGGAAATCAAGAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGT 2529
2538 AAATTGAGTCCATGGGGGAAATCAAGAGTGTCAAGTGTCAAGTGTCAAGTGTCAAGTGT 2587
2530 ATGTTTGTACACATGTGTACCTCACTGTCTCTGAAACTTGTGTGTGTGTGTGTGTGTGT 2589
2588 ATGTTTGTACACATGTGTACCTCACTGTCTCTGAAACTTGTGTGTGTGTGTGTGTGTGT 2647
2590 AGTCCACCTTCAATTAATCTTTTGAACCTGTATCATCTTTTGGCAAGTGAAGTGTGGGCT 2649
2648 AGTCCACCTTCAATTAATCTTTTGAACCTGTATCATCTTTTGGCAAGTGAAGTGTGGGCT 2707
2650 TATTTACAGTCTTGTGACAAATGAGTGGCTCTGACTTAAGCTTATTAATTAATTAATTAAT 2709
2708 TATTTACAGTCTTGTGACAAATGAGTGGCTCTGACTTAAGCTTATTAATTAATTAATTAAT 2767
2710 CTGAAGCAAAAGTGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2769
2768 CTGAAGCAAAAGTGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2827
2770 TCTGTGTCCTTCCCAATGCTGTGGGTTCACACAGAGGGAGGGTCCCTTTTGTGATGCTG 2829
2828 TCTGTGTCCTTCCCAATGCTGTGGGTTCACACAGAGGGAGGGTCCCTTTTGTGATGCTG 2887
2830 CAAGTGCATTAACATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2889
2888 CAAGTGCATTAACATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2947

2890 GTTTCGAAGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2949
2948 GTTTCGAAGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3007
2950 TGCATTCATTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3009
3008 TGCATTCATTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3067
3010 GGACCTTGAAGACATGTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 3069
3068 GGACCTTGAAGACATGTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 3127
3070 GTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3129
3128 GTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3187
3130 TTTGTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3189
3188 TTTGTCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3247
3190 CAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3249
3248 CAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3307
3250 TGAATGAGACAGCTCTCATTTCTTATTAAGGGGATGATGATGATGATGATGATGATGATG 3309
3308 TGAATGAGACAGCTCTCATTTCTTATTAAGGGGATGATGATGATGATGATGATGATGATG 3367
3310 ACCAATGATGAGGCAAGGCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3369
3368 ACCAATGATGAGGCAAGGCGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3426
3370 GCCTGCTCTGTTGAGAGAGTCCCTCAATGAGTCTCTTATTAATTAATTAATTAATTAAT 3426
3427 GCCTGCTCTGTTGAGAGAGTCCCTCAATGAGTCTCTTATTAATTAATTAATTAATTAAT 3483

RESULT 6
ABV27589
ID ABV27589 standard; cDNA; 3483 BP.
XX
AC ABV27589;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 27580.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
PN W0200160860-A2.
PD 23-AUG-2001.
XX
PD 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 5642-5643; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 3483 BP; 801 A; 860 C; 938 G; 884 T; 0 other;
Query Match 96.8%; Score 3331.8; DB 23; Length 3483;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3403; Conservative 0; Mismatches 7; Indels 7; Gaps 6;
QY 11 GGGCCAGTAGGCGGAGCTTAAGCAGAGGCGGAGGCGGAGGCGGAGGCGGAGG 70
Db 73 GGTGAGTAGGCGGAGCTTAAGCAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 132
QY 71 AGCGCGCGCTGGAGCGGCGGAGGCTATTTGAACTTCCAGATACCTATCTATCGAT 130
Db 133 AGCGCGCGCTGGAGCGGCGGAGGCTATTTGAACTTCCAGATACCTATCTATCGAT 192
QY 131 GCTGTGATTAACAGCAAGATGGCTTGAACACAGGCTCACCCGCGATTTGGAGCTTAC 190
Db 193 GCTGTGATTAACAGCAAGATGGCTTGAACACAGGCTCACCCGCGATTTGGAGCTTAC 252
QY 191 TATGAAACCATGATATCAACACCGGAAACCCCTATCCGACAGACCCGACTGTGCTCC 250
Db 253 TATGAAACCATGATATCAACACCGGAAACCCCTATCCGACAGACCCGACTGTGCTCC 312
QY 251 ACTGCTTACGAGGTGATCCGGCTCAGTACTACCGCTCCCGCTCCCGAGTACGCGCG 310
Db 313 ACTGCTTACGAGGTGATCCGGCTCAGTACTACCGCTCCCGCTCCCGAGTACGCGCG 372
QY 311 AGGGCTGAGGAGGAGGCTTCAACCCGCTGCTGACAGGCGGCAATCCCATCCGGG 370
Db 373 AGGGCTGAGGAGGAGGCTTCAACCCGCTGCTGACAGGCGGCAATCCCATCCGGG 432
QY 371 ACAGTGTGACCTCAAAAGACTAAGAAAGCACTGTGATCACCCTTGGGGAGCTTTC 430
Db 433 ACAGTGTGACCTCAAAAGACTAAGAAAGCACTGTGATCACCCTTGGGGAGCTTTC 492
QY 431 CTCGTGGAGAGCTGGCGCTGGCGCTTACTCTGGAAGTTTCATGGGAGCAAGTGTTC 490
Db 493 CTCGTGGAGAGCTGGCGCTGGCGCTTACTCTGGAAGTTTCATGGGAGCAAGTGTTC 552
QY 491 AACCTGGGATAGATGGAGCTTCAAGCTCAGGTACATCAACCCCTTAACTGGGTAT 550
Db 553 AACCTGGGATAGATGGAGCTTCAAGCTCAGGTACATCAACCCCTTAACTGGGTAT 612
QY 551 GGGCGTGCACATGCCCGGGGGAGAGAGAAATCGGTGTTCGCTCTACAGGACA 610
Db 613 GGGCGTGCACATGCCCGGGGGAGAGAGAAATCGGTGTTCGCTCTACAGGACA 672
QY 611 AACCTCATCTTCAAGGTCTACTCATCAGAGAAATCCTGGACCCCTGTGTCCAAAG 670
Db 673 AACCTCATCTTCAAGGTCTACTCATCAGAGAAATCCTGGACCCCTGTGTCCAAAG 732
QY 671 GACTGGAACGAACTAGGGGCGGGGCGCTGACAGGAGCAATGGGTATAAAGAAATTTT 730
Db 733 GACTGGAACGAACTAGGGGCGGGGCGCTGACAGGAGCAATGGGTATAAAGAAATTTT 792

QY 731 TACTCTAGCCAAAGAAATAGTGATGACAGCGGATCCACACCTTTATGAACGTGAACA 790
Db 733 TACTCTAGCCAAAGAAATAGTGATGACAGCGGATCCACACCTTTATGAACGTGAACA 852
QY 791 AGTGGCGGCAATGTGATATCTATTAATAAACTGTACCAAGTATGCTGTTCTTCAAA 850
Db 853 AGTGGCGGCAATGTGATATCTATTAATAAACTGTACCAAGTATGCTGTTCTTCAAA 912
QY 851 GCAGTGTTCCTTCAAGCTGTATACGCTGGGGGCACTTGAACCTCAAGCGCCAGAGC 910
Db 913 GCAGTGTTCCTTCAAGCTGTATACGCTGGGGGCACTTGAACCTCAAGCGCCAGAGC 972
QY 911 AGGATCGTGGGCGGAGAGCGCGCTCCCGGGGCGCTGCGGAGCTCAGCTTCA 970
Db 973 AGGATGTGGGCGGAGAGCGCGCTCCCGGGGCGCTGCGGAGCTCAGCTTCA 1031
QY 971 CGTCCAGAACGTCCACGCTGTGCGGAGGCTCCATCATCACCCCGAGTGTGACAGC 1030
Db 1032 CGTCCAGAACGTCCACGCTGTGCGGAGGCTCCATCATCACCCCGAGTGTGACAGC 1091
QY 1031 GCGCCACTGCGTGGAAAAACCTTAACAATCCATGCGATTTGGGGGAT 1090
Db 1092 GCGCCACTGCGTGGAAAAACCTTAACAATCCATGCGATTTGGGGGAT 1151
QY 1091 TTTGAGACAACTTTCATGTTCTATGAGCCGATACCAAGTAGAAAAAGTATTTCA 1150
Db 1152 TTTGAGACAACTTTCATGTTCTATGAGCCGATACCAAGTAGAAAAAGTATTTCA 1211
QY 1151 TTCAATTTATGACTCCAAAGACCAAGAACATGACATTCGCTGATGAAGCTGACAGACC 1210
Db 1212 TTCAATTTATGACTCCAAAGACCAAGAACATGACATTCGCTGATGAAGCTGACAGACC 1271
QY 1211 TCTGACTTTCACAGCACTAGTGAACCAAGTGTGCTGCCAACCCAGCATGATGCTCA 1270
Db 1272 TCTGACTTTCACAGCACTAGTGAACCAAGTGTGCTGCCAACCCAGCATGATGCTCA 1331
QY 1271 GCCAGAACAGCTCTGCTGATTTCCGGGTGGGGGCGCCACGAGAGAAAGGAGACCTC 1330
Db 1332 GCCAGAACAGCTCTGCTGATTTCCGGGTGGGGGCGCCACGAGAGAAAGGAGACCTC 1391
QY 1331 AGAAGTGTGAACGCTGCCAAGGTGCTTCTCATTTGACACAGAGATGCAACAGCATTA 1390
Db 1392 AGAAGTGTGAACGCTGCCAAGGTGCTTCTCATTTGACACAGAGATGCAACAGCATTA 1451
QY 1391 TGTCTATGACAACCTGATCACACACGATATGTCGCGGCTTCCTCGAGGGGAAGT 1450
Db 1452 TGTCTATGACAACCTGATCACACACGATATGTCGCGGCTTCCTCGAGGGGAAGT 1511
QY 1451 CGATTCTTGCCAGGCTGACAGTGAAGGCGCTGTGCTCACTTCAAGAAACAATATCTGCTG 1510
Db 1512 CGATTCTTGCCAGGCTGACAGTGAAGGCGCTGTGCTCACTTCAAGAAACAATATCTGCTG 1571
QY 1511 GCTGATAGGGATACAGCTGGGGTTCGCTGTGCTCCAAAGCTTACAGACAGAGTGA 1570
Db 1572 GCTGATAGGGATACAGCTGGGGTTCGCTGTGCTCCAAAGCTTACAGACAGAGTGA 1631
QY 1571 CGGGAATGATGATGATTAACGAGTGAATTTATGCAAAATGAGGGAGAGCGGTATTC 1630
Db 1632 CGGGAATGATGATGATTAACGAGTGAATTTATGCAAAATGAGGGAGAGCGGTATTC 1691
QY 1631 CACATGCTCTTCTGCTTACAGCTGCTTTTACAGAAAAACAATGGGCGCTTTTGTCTCC 1690
Db 1692 CACATGCTCTTCTGCTTACAGCTGCTTTTACAGAAAAACAATGGGCGCTTTTGTCTCC 1751
QY 1691 CCGTGCATGATTTACTCTTAAAGATGATTCAGAGTCACTTCAATTTTATTAACAGTGA 1750
Db 1752 CCGTGCATGATTTACTCTTAAAGATGATTCAGAGTCACTTCAATTTTATTAACAGTGA 1811
QY 1751 ACTTGTCTGCTTGGGCACTCTGCTCCATTCCTGTCAGAGGTGAGTGGCTCCCTGGCCA 1810
Db 1812 ACTTGTCTGCTTGGGCACTCTGCTCCATTCCTGTCAGAGGTGAGTGGCTCCCTGGCCA 1871

1811 GCCTGCTCCCTAACCCCTGTCCGCAAGGGTATGGCCGGCTGGTTGTGGGCACTGG 1870
 Db 1872 GCTCTCTCCCTAACCCCTGTCCGCAAGGGTATGGCCGGCTGGTTGTGGGCACTGG 1931
 1871 CGGTCAAGGTGAGAGAGAGGGGTGGAGGCTGCCCATTTGAGATCTCTCTGCTGATTCCT 1930
 Db 1932 CGGTCAAGGTGAGAGAGAGGGGTGGAGGCTGCCCATTTGAGATCTCTCTGCTGATTCCT 1991
 1931 TTCCAGGGGCCAATTTTGGATGAGCATGAGCTGTACCTCTCAGCTGCTGATGACTGG 1990
 Db 1992 TTCCAGGGGCCAATTTTGGATGAGCATGAGCTGTACCTCTCAGCTGCTGATGACTGG 2051
 1991 AGATCAAAAAAGAGAGACATGAGAAAGGAGACAGCCAGGTGGCAGCTGCAGCGCTG -CC 2049
 Db 2052 AGATCAAAAAAGAGAGACATGAGAAAGGAGAGACAGCCAGGTGGCAGCTGCAGCGCTGC 2111
 2050 TCTGGGGCCACTTGGTATGCTCCCAAGCTTACCTCCCAAGGGGATTTTGTGATGGG 2109
 Db 2112 TCTGGGGCCACTTGGTATGCTCCCAAGCTTACCTCCCAAGGGGATTTTGTGATGGG 2171
 2110 TTCTTAGAGACCTTAGCAGCCCTGATGTGGCCAGAAATTAAGGACAGCCCTTCATGG 2169
 Db 2172 TTCTTAGAGACCTTAGCAGCCCTGATGTGGCCAGAAATTAAGGACAGCCCTTCATGG 2231
 2170 GTGTGACGTGGTATGACCTTTGTAAGGGGAAAGAAACATTTTGTCTATGAGGTGA 2229
 Db 2232 GTGTGACGTGGTATGACCTTTGTAAGGGGAAAGAAACATTTTGTCTATGAGGTGA 2290
 2230 GAATTTACACAGTCCCTGGGTGGGAGGAGCAATTGAAAGAACTTTGCCCTTAGGA 2289
 Db 2291 GAATTTACACAGTCCCTGGGTGGGAGGAGCAATTGAAAGAACTTTGCCCTTAGGA 2349
 2290 CTCTGTGTGAGAGTGTCCACCTGACATTTGGGGGCTCTGAGGAGAGACTAGCCT 2349
 Db 2350 CTCTGTGTGAGAGTGTCCACCTGACATTTGGGGGCTCTGAGGAGAGACTAGCCT 2409
 2350 TCTCTCTACCTCTCCCTGACCTGCTCTAGCACTTGGAGAGTGCATATGCCCTTGGT 2409
 Db 2410 TCTCTCTACCTCTCCCTGACCTGCTCTAGCACTTGGAGAGTGCATATGCCCTTGGT 2469
 2410 COTGGGCAAGGGGGGCAAGTGTGGGCAACATTTGGGCTTTTACAGGCTCTGATGACTGG 2469
 Db 2470 COTGGGCAAGGGGGGCAAGTGTGGGCAACATTTGGGCTTTTACAGGCTCTGATGACTGG 2527
 2470 AAATTGAGGTCCATGGGGGAAATCAAGAGTCTCAGTTAAGTTAAGTACATGTTTCCATGTT 2529
 Db 2528 AAATTGAGGTCCATGGGGGAAATCAAGAGTCTCAGTTAAGTTAAGTACATGTTTCCATGTT 2587
 2530 ATGTTTCTACACATTTGCTACCTGCTGCTGAGAACTTTAGCTTTGATGCTCCAGT 2589
 Db 2588 ATGTTTCTACACATTTGCTACCTGCTGCTGAGAACTTTAGCTTTGATGCTCCAGT 2647
 2590 AGTCACCTCTCATTAACCTTTGAAACGTATCATCTTTGGCACTAGAGTGGTGGCC 2649
 Db 2648 AGTCACCTCTCATTAACCTTTGAAACGTATCATCTTTGGCACTAGAGTGGTGGCC 2707
 2650 TATTTACAGTCTTTGACAAATGACTGCTCCTGACTTAAGCTTATTAATGATGTTG 2709
 Db 2708 TATTTACAGTCTTTGACAAATGACTGCTCCTGACTTAAGCTTATTAATGATGTTG 2767
 2710 CTGAAGCAAAAGTGGCCATGCTGGGGGCGAAGAAAGAAAGATGTTGTTTGGAGTCT 2769
 Db 2768 CTGAAGCAAAAGTGGCCATGCTGGGGGCGAAGAAAGATGTTGTTTGGAGTCT 2827
 2770 TCTGAGTCCCTTCAAAAGCTGTTGGGTTTCAACCAAGGGGAGGGCTTTTGGCACTGG 2829
 Db 2828 TCTGAGTCCCTTCAAAAGCTGTTGGGTTTCAACCAAGGGGAGGGCTTTTGGCACTGG 2887
 2830 CAAGTCCATTAACATGAGCACTACTCTACATGTTTCTGCTCTGCGCAAGCAGCTG 2889
 Db 2888 CAAGTCCATTAACATGAGCACTACTCTACATGTTTCTGCTCTGCGCAAGCAGCTG 2947
 2890 GTTTCAGAGATGAATGAATGATGATCTACAGCTAGAGCTTAACTTGAAATGAAAGTCT 2949

Db 2948 GTTTCAGAGATGAATGAATGATGATCTACAGCTAGAGACTTAACCTTGAAATGAAAGTCT 3007
 2950 TGCATCCCATTTGACAGATCCGCTGTGACATAGCCTGCTGAGAGGAGCAATTCGCG 3009
 Db 3008 TGCATCCCATTTGACAGATCCGCTGTGACATAGCCTGCTGAGAGGAGCAATTCGCG 3067
 3010 GGACCTTGGAAACAGTTGGCACTGTAAAGTGTGCTGCCCAAGACACATCTTAAAGGT 3069
 Db 3068 GGACCTTGGAAACAGTTGGCACTGTAAAGTGTGCTGCCCAAGACACATCTTAAAGGT 3127
 3070 GTTGTATGTTGTAAGACGTCCTCTCTTATTTATGCCCCCTCTTATTTATGTAACAAC 3129
 Db 3128 GTTGTATGTTGTAAGACGTCCTCTCTTATTTATGCCCCCTCTTATTTATGTAACAAC 3187
 3130 TTTGTCTTTTGTGTAAGTCTTTTAAAGCTGTAAGTTCATATGTTGTAAGTTCATATG 3189
 Db 3188 TTTGTCTTTTGTGTAAGTCTTTTAAAGCTGTAAGTTCATATGTTGTAAGTTCATATG 3247
 3190 CAATTAATTTATGCAATTTTCTTCAAGTAACCACTGATCTTGAAGTTCGCTGG 3249
 Db 3248 CAATTAATTTATGCAATTTTCTTCAAGTAACCACTGATCTTGAAGTTCGCTGG 3307
 3250 TGAATGAGACCACTTCATTTCTTATTAAGGGGTGATGTTAGGCTGCTGAGAG 3309
 Db 3308 TGAATGAGACCACTTCATTTCTTATTAAGGGGTGATGTTAGGCTGCTGAGAG 3367
 3310 ACCAAGGTGAGGCAAGGCGCAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 3369
 Db 3368 ACCAAGGTGAGGCAAGGCGCAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 3426
 3370 GCCTGTCTGTTGAGAGAGTCCCTCAATGACTCTCTTATTTATTTATTTAGTCTG 3426
 Db 3427 GCCTGTCTGTTGAGAGAGTCCCTCAATGACTCTCTTATTTATTTATTTAGTCTG 3483

RESULT 7
 ABV29119
 ID ABV29119 standard; cDNA; 3483 BP.
 XX
 AC ABV29119;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 29110.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 PD 23-AUG-2001.
 XX
 PD 20-FEB-2001; 2001WO-US05171.
 PF 17-FEB-2000; 2000US-183139P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer

XX Claim 1: Page 6183-6184; 11750bp; English.
PS
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV2213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) determining the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 3483 bp; 801 A; 860 C; 938 G; 884 T; 0 other;

Query Match 96.8%; Score 3331.8; DB 23; Length 3483;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3403; Conservative 0; Mismatches 7; Indels 7; Gaps 6;

QY 11 GCGCGAGTAGGCGGAGCTAAGACAGAGCGGAGCGGAGCGGAGGCGGAGGCGG 70
DB 73 GGTGAGTAGGCGGAGCTAAGACAGAGCGGAGCGGAGCGGAGGCGGAGGCGG 132
QY 71 AGCGCGCGCTGGAGCGGCGGAGCTATTTAATCAATTCCTATCTATCTGAT 130
DB 133 AGCGCGCGCTGGAGCGGCGGAGCTATTTAATCAATTCCTATCTATCTGAT 192
QY 131 GCTGTGATTAACAGCAAGATGGCTTTGAACACAGGCTCACACAGCAATTTGACCTTAC 190
DB 193 GCTGTGATTAACAGCAAGATGGCTTTGAACACAGGCTCACACAGCAATTTGACCTTAC 252
QY 191 TATGAAAAACATGATACCAACCGAAAAACCCATATCCGACACAGCCCATGTGTCCC 250
DB 253 TATGAAAAACATGATACCAACCGAAAAACCCATATCCGACACAGCCCATGTGTCCC 312
QY 251 ACTGTCTACAGAGTGCATCCGGCTCAGTACTACCCGCTCCCGCTCCCGCTACGAGCCCG 310
DB 313 ACTGTCTACAGAGTGCATCCGGCTCAGTACTACCCGCTCCCGCTCCCGCTACGAGCCCG 372
QY 311 AGGCTCTGACGAGGCTTCCAAACCGCTGCTGACAGCAGCCCAATTTCCCATCCGG 370
DB 373 AGGCTCTGACGAGGCTTCCAAACCGCTGCTGACAGCAGCCCAATTTCCCATCCGG 432
QY 371 ACAGTGTGACACCTCAAGACTAAGAAAGCACTGTGCATCACCTTGACCTGGGACCTTC 430
DB 433 ACAGTGTGACACCTCAAGACTAAGAAAGCACTGTGCATCACCTTGACCTGGGACCTTC 492
QY 431 CTCGTGGAGAGTGGCGCTGGCGCTGCTACTCTGGAAGTTCAATGGGAGCAAGTGTCC 490
DB 493 CTCGTGGAGAGTGGCGCTGGCGCTGCTACTCTGGAAGTTCAATGGGAGCAAGTGTCC 552
QY 491 AACCTGGATAGAGTGGAGCTCTCAGTACCTGCATCAACCCCTTAACCTGGTGTAT 550
DB 553 AACCTGGATAGAGTGGAGCTCTCAGTACCTGCATCAACCCCTTAACCTGGTGTAT 612
QY 551 GCGGTGTACACCTCCCGCGGAGGAGACAGATGGTGTGTTCGCTCTACGAGCA 610
DB 613 GCGGTGTACACCTCCCGCGGAGGAGACAGATGGTGTGTTCGCTCTACGAGCA 672
QY 611 AACCTTCATCTTCAAGTGTACTCATCTCAGAGAAAGTCTTGACACCTGTGTCCAGAC 670
DB 673 AACCTTCATCTTCAAGTGTACTCATCTCAGAGAAAGTCTTGACACCTGTGTCCAGAC 732
QY 671 GACTGGAACGAGCACTACGGGCGGCGGCTGACAGGAGCATGGGTATTAAGAAATATTTT 730
DB 733 GACTGGAACGAGCACTACGGGCGGCGGCTGACAGGAGCATGGGTATTAAGAAATATTTT 792

QY 731 TACTCTAGCCAAAGAAATAGTGATGACAGCGGATCCACACCTTTATGAACGTGAACA 790
DB 793 TACTCTAGCCAAAGAAATAGTGATGACAGCGGATCCACACCTTTATGAACGTGAACA 852
QY 791 AGTCCGGCATGTGATATCTATATAAAACTGTACACAGTGAAGCTGTCTTCAAAA 850
DB 853 AGTCCGGCATGTGATATCTATATAAAACTGTACACAGTGAAGCTGTCTTCAAAA 912
QY 851 GCAGGTGTTCTTTACGCTGTATACCTGCGGGGCACTTGAACCTCAAGCGGACAGC 910
DB 913 GCAGGTGTTCTTTACGCTGTATACCTGCGGGGCACTTGAACCTCAAGCGGACAGC 972
QY 911 AGATGTGGGCGGAGAGCGGCTCCCGGGGCGCTGCTGGGAGGTGACGCTTCA 970
DB 973 AGATGTGGGCGGAGAGCGGCTCCCGGGGCGCTGCTGGGAGGTGACGCTTCA 1031
QY 971 CGTCCAGAACGTCCACGCTGTGCGGAGGCTCCATATCAACCCCGAGTGTGATCGACAGC 1030
DB 1032 CGTCCAGAACGTCCACGCTGTGCGGAGGCTCCATATCAACCCCGAGTGTGATCGACAGC 1091
QY 1031 CGCCCACTGCGTGAAGAAACCTTTAACAATTCATGAGCATTTGAGCGGATTTGGGGAT 1090
DB 1092 CGCCCACTGCGTGAAGAAACCTTTAACAATTCATGAGCATTTGAGCGGATTTGGGGAT 1151
QY 1091 TTTGAGACAATCTTTATGATGTTCTATGAGCCGATACCAAGTAGAAAAAGTATTTCTCA 1150
DB 1152 TTTGAGACAATCTTTATGATGTTCTATGAGCCGATACCAAGTAGAAAAAGTATTTCTCA 1211
QY 1151 TCCAAATTAATGATCTCAAGACCAAGAACATGACATTTGCGCTGATGAGCTGACAAACC 1210
DB 1212 TCCAAATTAATGATCTCAAGACCAAGAACATGACATTTGCGCTGATGAGCTGACAAACC 1271
QY 1211 TCTGACTTTCAACGACCTAGTGAACCAAGTGTGTGCGCAACCCAGGCTGATGCTGCA 1270
DB 1272 TCTGACTTTCAACGACCTAGTGAACCAAGTGTGTGCGCAACCCAGGCTGATGCTGCA 1331
QY 1271 GCCAGAACGCTGTGCTGATTTCCGGGTGGGGGCCACGAGAGAAAGGAAACCTC 1330
DB 1332 GCCAGAACGCTGTGCTGATTTCCGGGTGGGGGCCACGAGAGAAAGGAAACCTC 1391
QY 1331 AGAAGTGTGAACGCTGCCAAGGTCTTCTCATTTAGACACAGAGATGCAACAGACATTA 1390
DB 1392 AGAAGTGTGAACGCTGCCAAGGTCTTCTCATTTAGACACAGAGATGCAACAGACATTA 1451
QY 1391 TGTCTATGACAACTGATACACACGACCATGATGTGCTCCGCTTCCGAGGGAACT 1450
DB 1452 TGTCTATGACAACTGATACACACGACCATGATGTGCTCCGCTTCCGAGGGAACT 1511
QY 1451 CGATTCTTGCCAGGAGTGAAGTGAAGGCGCTGTGTCACTTGAAGAAACAATATCTGGTG 1510
DB 1512 CGATTCTTGCCAGGAGTGAAGTGAAGGCGCTGTGTCACTTGAAGAAACAATATCTGGTG 1571
QY 1511 GCTGATTAAGGATACAACTGGGGTTCGTGCTGTGCCAAAGCTTACACACAGAGTGT 1570
DB 1572 GCTGATTAAGGATACAACTGGGGTTCGTGCTGTGCCAAAGCTTACACACAGAGTGT 1631
QY 1571 CGGGAATGATGATGATTTACAGGACTGATTTATGCAAAATGAGGGAGAGAGGCTAATC 1630
DB 1632 CGGGAATGATGATGATTTACAGGACTGATTTATGCAAAATGAGGGAGAGAGGCTAATC 1691
QY 1631 CACATGATCTTCTGCTGCTGAGCTGTTTACAGAAAAAATGGGCTGTTTCTTCC 1690
DB 1692 CACATGATCTTCTGCTGCTGAGCTGTTTACAGAAAAAATGGGCTGTTTCTTCC 1751
QY 1691 CCGTGCATGATTTACTCTTACAGATGATTCAGAGTCACTTCATTTTATTAACAGTGA 1750
DB 1752 CCGTGCATGATTTACTCTTACAGATGATTCAGAGTCACTTCATTTTATTAACAGTGA 1811
QY 1751 ACTTGCTGGGCTTGGGACCTGCTGCAATTCGTCAGAGGCTGCAAGTGGCTCCCGGCCCA 1810
DB 1812 ACTTGCTGGGCTTGGGACCTGCTGCAATTCGTCAGAGGCTGCAAGTGGCTCCCGGCCCA 1871
QY 1811 GCTTGCTCTCCCTAACCCCTTGTGCGCAAGGAGTGAAGGCGGCTGTGTGGGCACTGG 1870


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|||||
Db 1872 GCGTCTCTCCCTAAACCCCTGTCCGAAGGGGTGATGGCCGGCTGGTGTGGGAGCTGG 1931
Qy 1871 CGGTCAAGTGTGAGAGAGAGGGGTGGAGGCTGGCCCATTTGAGATCTTCCCTGTGATGCT 1930
Db 1932 CGGTCAAGTGTGAGAGAGAGGGGTGGAGGCTGGCCCATTTGAGATCTTCCCTGTGATGCT 1931
Qy 1931 TTCCAGGGGCCAAATTTTGGATGAGCATGAGCTGTACCTCTCACTCTGATGATGATG 1990
Db 1992 TTCCAGGGGCCAAATTTTGGATGAGCATGAGCTGTACCTCTCACTCTGATGATGATG 2051
Qy 1991 AGATCAAAAAAGAGAGAGATGGAAGAGAGACAGCAGGAGGTGGCAGCTGAGGCGCTG -CC 2049
Db 2052 AGATCAAAAAAGAGAGAGATGGAAGAGAGACAGCAGGAGGTGGCAGCTGAGGCGCTG 2111
Qy 2050 TCTGGGGCCACTTGGTGTAGTGTGCCAGGCTACCTCTCCACAAGGGGATTTTCTGATGG 2109
Db 2112 TCTGGGGCCACTTGGTGTAGTGTGCCAGGCTACCTCTCCACAAGGGGATTTTCTGATGG 2171
Qy 2110 TTCTTAGAGCCTTAGCAGCCCTGATGGTGGCCAGAAAATAAGGGAGCAGCCCTTCATGG 2169
Db 2172 TTCTTAGAGCCTTAGCAGCCCTGATGGTGGCCAGAAAATAAGGGAGCAGCCCTTCATGG 2231
Qy 2170 GTGGGAGGTGGTGTACCTTGTGAAGGGGAACAGAAACATTTTGTCTTATGGGTGA 2229
Db 2232 GTGGGAGGTGGTGTACCTTGTGAAGGGGAACAGAAACATTTTGTCTTATGGGTGA 2290
Qy 2230 GAATATAGACAGTGGCTTGGGTGGAGGGAAGCAATTTGAAAAGAACTTGGCCCTGAGCA 2289
Db 2291 GAATATAGACAGTGGCTTGGGTGGAGGGAAGCAATTTGAAAAGAACTTGGCCCTGAGCA 2349
Qy 2290 CTCCGTGGTGGAGTCTCCACCTGCACATTTGGGTGGGCTCTGGAGGAGAGACTGAGCT 2349
Db 2350 CTCCGTGGTGGAGTCTCCACCTGCACATTTGGGTGGGCTCTGGAGGAGAGACTGAGCT 2409
Qy 2350 TCCCTCTATCTCTCCCTACCCCTGCTCTAGACCCCTGGAAGTGCACATGCCCTTGCT 2409
Db 2410 TCCCTCTATCTCTCCCTACCCCTGCTCTAGACCCCTGGAAGTGCACATGCCCTTGCT 2469
Qy 2410 CCTGGGAGGGGGCCAGATGTGGCACCATGTGGGCTCTTTAGGCTGCTATGACTGG 2469
Db 2470 CCTGG - CAGGGGGCCAGATGTGGCACCATGTGGGCTCTTTAGGCTGCTATGACTGG 2527
Qy 2470 AAATTTAGCTCCATGGGGAAATCAAGATGCTCAGTTTAAAGTACACTGTTTCCATGT 2529
Db 2528 AAATTTAGCTCCATGGGGAAATCAAGATGCTCAGTTTAAAGTACACTGTTTCCATGT 2587
Qy 2530 ATGTTTCTACACATTTGCTACCTGATGCTCTCGGAAACTTATGATGCTCTCCAGT 2589
Db 2588 ATGTTTCTACACATTTGCTACCTGATGCTCTCGGAAACTTATGATGCTCTCCAGT 2647
Qy 2590 AGTCACCTTATTTACTCTTTTGAACGTATCATCTTTGGCAAGTAAAGATGGGGC 2649
Db 2648 AGTCACCTTATTTACTCTTTTGAACGTATCATCTTTGGCAAGTAAAGATGGGGC 2707
Qy 2650 TATTTACGCTCTTTGACAAAATGACTGGCTCTGACTTAACGTTCTATAATGATGTG 2709
Db 2708 TATTTACGCTCTTTGACAAAATGACTGGCTCTGACTTAACGTTCTATAATGATGTG 2767
Qy 2710 CTGAAGCAAAATGTGGCCATGTTGGGGCCGGAAGAAGAAAGATGTGTTTGTGGAGCT 2769
Db 2768 CTGAAGCAAAATGTGGCCATGTTGGGGCCGGAAGAAGAAAGATGTGTTTGTGGAGCT 2827
Qy 2770 TCTGTGTCCTCTCAATGCTGTGGTTTCCAAACAGGGGGAAGGGTCCCTTTGATTCG 2829
Db 2828 TCTGTGTCCTCTCAATGCTGTGGTTTCCAAACAGGGGGAAGGGTCCCTTTGATTCG 2887
Qy 2830 CAAGTCCATTAACATGAGCACTACTTACATGATGTTCTGCTCTGGCCAGAGGCTG 2889
Db 2888 CAAGTCCATTAACATGAGCACTACTTACATGATGTTCTGCTCTGGCCAGAGGCTG 2947
Qy 2890 GTTTGCAAGATGAAATGATGATTTCTACAGCTAGGACTTAACCTTGAATGGAAGTCT 2949
|||||

Db 2948 GTTTGCAAGATGAAATGATGATTTCTACAGCTAGGACTTAACCTTGAATGGAAGTCT 3007
Qy 2950 TGCATCCCATTTTGCAGATCCGCTGTGCACATGCCCTGTGAGAGAGCATTTCCAG 3009
Db 3008 TGCATCCCATTTTGCAGATCCGCTGTGCACATGCCCTGTGAGAGAGCATTTCCAG 3067
Qy 3010 GGAACCTTGAACAGTTGGCACTGTAAAGTGTCTGCTCCCAAGACATCTTAAAGGT 3069
Db 3068 GGAACCTTGAACAGTTGGCACTGTAAAGTGTCTGCTCCCAAGACATCTTAAAGGT 3127
Qy 3070 GTTGTAAAGTGAACAGTCTCTCTCTTATTTGCCCCCTCTTATTTATGTAACAAGT 3129
Db 3128 GTTGTAAAGTGAACAGTCTCTCTCTTATTTGCCCCCTCTTATTTATGTAACAAGT 3187
Qy 3130 TTTGTCTTTTGTATCTTTTAACTGTAAAGTCAATGTGAATGAAATATCATG 3189
Db 3188 TTTGTCTTTTGTATCTTTTAACTGTAAAGTCAATGTGAATGAAATATCATG 3247
Qy 3190 CAAATTAATTAAGCAGTTTCTTCAAGTAACACATGCATCTTGAAGTCTGCTGG 3249
Db 3248 CAAATTAATTAAGCAGTTTCTTCAAGTAACACATGCATCTTGAAGTCTGCTGG 3307
Qy 3250 TGAGTAGACACAGCTTCCATTTCTTATTAAGGGGTGATGTAGGCTGCTGACAGG 3309
Db 3308 TGAGTAGACACAGCTTCCATTTCTTATTAAGGGGTGATGTAGGCTGCTGACAGG 3367
Qy 3310 ACCAAAGTGAAGGACAGGACAGCTGTGCTCTGCTGGTGGTGGCCCTCAGTCTCGA 3369
Db 3368 ACCAAAGTGAAGGACAGGACAGCTGTGCTCTGCTGGTGGTGGCCCTCAGTCTCGA 3426
Qy 3370 GCCGTCTCTGTTGGAGAGGTGCCCTCAATGACTCTTCTTATTTCTATTACTGTG 3426
Db 3427 GCGTGTCTGTTGGAGAGGTGCCCTCAATGACTCTTCTTATTTCTATTACTGTG 3483

RESULT 8
ABV24651
ID ABV24651 standard; cDNA; 3483 BP.
XX
AC ABV24651;
XX
AC
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 24642.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JB;
XX
PI WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
```


Db	1872	GCATGCTCCCTAACACCCCTTGTTCGCCAAG666GTATATGGCCGCGTGTGTGGGACACTGG	1931
Oy	1871	CGGTCAAGTGTGGAGAGAGGGGTGGAGGCTGCCCCATTGAGATCTTCTGCTGAGTCT	1930
Db	1932	CGGTCAAGTGTGGAGAGAGGGGTGGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCT	1991
Oy	1931	TTTCCAGGGGCGCAATTTTGGATGAGCATTTGAGACTGTTCACCTTCACACTGCTGGATGACTTG	1990
Db	1992	TTTCCAGGGGCGCAATTTTGGATGAGCATTTGAGACTGTTCACCTTCACACTGCTGGATGACTTG	2051
Oy	1991	AGATGAAAAAGSAGAGACATGAGAAAGGAGACAGCCAGTGGCACCTGCACGGCTG - CC	2049
Db	2052	AGATGAAAAAGSAGAGACATGAGAAAGGAGACAGCCAGTGGCACCTGCACGGCTGCC	2111
Oy	2050	TCTGGGGCCACTTGGTAGTGTCCCAAGCCTACCTCTCCACAAGGGGATTTGCTGATGG	2109
Db	2112	TCTGGGGCCACTTGGTAGTGTCCCAAGCCTACCTCTCCACAAGGGGATTTGCTGATGG	2171
Oy	2110	TTTCTTAAGCCTTAAGCAGCCCTTGGATGTGGCCAGAAATAAAGGACACAGCCCTTCATGG	2169
Db	2172	TTTCTTAAGCCTTAAGCAGCCCTTGGATGTGGCCAGAAATAAAGGACACAGCCCTTCATAGG	2231
Oy	2170	GTGTGACGCTGGTAGTACCTGTGAAGGGGAAACAGAAATTTTGTCTATAGGGGGA	2229
Db	2232	GTGTGACGCTGGTAGTCT - CTTTAAAGGGGAACAGAAATTTTGTCTATAGGGGGA	2290
Oy	2230	GAATATAGACAGTGCCTTTGGGTGCGAGGGGAAGCAATTTGAAAGGACCTGCCCTGAGCA	2289
Db	2291	GAATATAGACAGTGCCTT - GGTGAGAGGGAAAGCAATTTGAAAGGACCTGCCCTGAGCA	2349
Oy	2290	CTCTGGTGCAGAGTCTTCACCTGCACATTTGGGTGGGGCTCTGGGAGGAGACTCAGCT	2349
Db	2350	CTCTGGTGCAGAGTCTTCACCTGCACATTTGGGTGGGGCTCTGGGAGGAGACTCAGCT	2409
Oy	2350	TCCCTCCATCTCCCTGACCCGACCTGTGCTCCTAAGACCCCTGGAGGTGTCACATGCCCTTGGT	2409
Db	2410	TCTCTCTCATCTCTCCGACCCGCTCTCTAAGCACCCCTGGAGGTGTCACATGCCCTTGGT	2469
Oy	2410	CCGTGGGAGGGGGCCCAAGTCTGTGCACCAATGTTGGGCTCTTAGGCTCTGTAAGTCACTGG	2469
Db	2470	CCGTGG - CAGGGGGCCAAAGTCTGGACACCAATGTTGGGCTCTTAGGCTCTGTAAGTCACTGG	2527
Oy	2470	AAATTTAGGCTCATTTAGCTTTGAAGCAATGCTCAGTTTAAAGTCACTGTTCCATGTT	2529
Db	2528	AAATTTAGGCTCATTTAGCTTTGAAGCAATGCTCAGTTTAAAGTCACTGTTCCATGTT	2587
Oy	2530	ATGTTTACACATTTGCTACCTCAGTCAAGTGCCTGGAAACTTACCTTTATGTCGCCAAGT	2589
Db	2588	ATGTTTACACATTTGCTACCTCAGTCAAGTGCCTGGAAACTTACCTTTATGTCGCCAAGT	2647
Oy	2590	AGTCCACCTTCATTTAACTCTTTGAAGCAATGTCATCTTTGCAAGTAAAGTGGTGGC	2649
Db	2648	AGTCCACCTTCATTTAACTCTTTGAAGCAATGTCATCTTTGCAAGTAAAGTGGTGGC	2707
Oy	2650	TATTTCAAGTCTTTGACAAATGACTGCTCCGACTTAAAGTCTATAATGAAATGTG	2709
Db	2708	TATTTCAAGTCTTTGACAAATGACTGCTCCGACTTAAAGTCTATAATGAAATGTG	2767
Oy	2710	CTGAAGCAAAAGTGGCCATTTGGTGGGGCCGAAAGAAAGAAAGATGTGTTTGTGTTGGATC	2769
Db	2768	CTGAAGCAAAAGTGGCCATTTGGTGGGGCCGAAAGAAAGAAAGATGTGTTTGTGTTGGATC	2827
Oy	2770	TCTGTGGTCCCTTCACATGTGTGGGTTTTCACAACAGGGGAAGGGTCCCTTTGCAATGC	2829
Db	2828	TCTGTGGTCCCTTCACATGTGTGGGTTTTCACAACAGGGGAAGGGTCCCTTTGCAATGC	2887
Oy	2830	CAAGTGCATTAACCATGAGCACTACTCTACCATGTTGTCCTCTCTGGCCAAAGAGCTG	2889
Db	2888	CAAGTGCATTAACCATGAGCACTACTCTACCATGTTGTCCTCTCTGGCCAAAGAGCTG	2947
Oy	2890	GTTTTCGCAAGATGAATGATGTTCTAAGAGTAGAGACTTAACTTTGAAATGGAAGTCT	2949
Db	2948	GTTTTCGCAAGATGAATGATGTTCTAAGAGTAGAGACTTAACTTTGAAATGGAAGAGTCT	3007

QY	2950	TCGATCCCATTTGGAGAGATCCGTCGTGGCAATGCGCTGTGAGAGACAGCATTCGAC	3009
QY	3008	TGCAATCCCATTTGGAGAGATCCGTCGTGGCAATGCGCTGTGAGAGAGAGCATTCGAC	3067
QY	3010	GGACCTTGGAAACACATTGGACACTGTAAAGTGGCTTGCTCCCAAGACACATCCATAAAGT	3069
Db	3068	GGACCTTGGAAACACATTGGACACTGTAAAGTGGCTTGCTCCCAAGACACATCCATAAAGT	3127
QY	3070	GTTGTAATGGTGAAGAAACGCTCTCTCTTATTTATGCCCCCTCTTATTATGTAACACTG	3129
Db	3128	GTTGTAATGGTGAAGAAACGCTCTCTCTTATTTATGCCCCCTCTTATTATGTAACACTG	3187
QY	3130	TTTGCTTTTTTTTGTATCTTTTTTAAACGTAAAGTCAATTGAATGCAAAATGAATATCAG	3189
Db	3188	TTTGCTTTTTTTTGTATCTTTTTTAAACGTAAAGTCAATTGAATGCAAAATGAATATCAG	3247
QY	3190	CAAAATAAATTATGACATTTTTTTTCAAAAGTAACACATGCATCTTTGAAGTCTGCTCG	3249
Db	3248	CAAAATAAATTATGACATTTTTTTTCAAAAGTAACACATGCATCTTTGAAGTCTGCTCG	3307
QY	3250	TGAGTAGGACACAGCTCCATTTCTTATTAAGGGGTATGTTGAGGCTGTGCTGACAGG	3309
Db	3308	TGAGTAGGACACAGCTCCATTTCTTATTAAGGGGTATGTTGAGGCTGTGCTGACAGG	3367
QY	3310	ACCAAGGAGGACGAAGGACAGCTTGGTGCCTCGTGGTGGTGCCCGCACTTCGCA	3369
Db	3368	ACCAAGGAGGACGAAGGACAGCTTGGTGCCTCGTGGTGGTGCCCGCACTTCGCA	3426
QY	3370	GCGTGTCCCTGTTGGAGAGGTCCTCCCAAAATGACATCCCTTATTATTAATTAAGTCTG	3426
Db	3427	GCGTGTCCCTGTTGGAGAGGTCCTCCCAAAATGACATCCCTTATTATTAATTAAGTCTG	3483
RESULT 9			
ABV29165			
ID	ABV29165	standard; cDNA; 3483	BP.
XX	AC	ABV29165;	
XX	DT	16-SEP-2002	(first entry)
XX	DE	Human prostate expression marker	cdNA 29156.
XX	KM	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker	
XX	KW	pharmacogenomic marker; gene; ss.	
XX	OS	Homo sapiens.	
XX	PN	WO200160860-A2.	
XX	PD	23-AUG-2001.	
XX	PF	20-FEB-2001; 2001WO-US05171.	
XX	PR	17-FEB-2000; 2000US-183319P.	
XX	PR	16-MAR-2000; 2000US-189862P.	
XX	PR	25-MAY-2000; 2000US-207454P.	
XX	PR	09-JUN-2000; 2000US-211314P.	
XX	PR	18-JUL-2000; 2000US-219007P.	
XX	PR	13-DEC-2000; 2000US-255281P.	
PA		(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX	PI	Schlegel R, Endege WO, Monahan JE;	
XX	DR	WPI; 2001-662795/76.	
XX	PT	Novel isolated nucleic acid molecule associated with cancerous state of	
XX	PT	prostate cells and correlating with presence of prostate cancer, useful	
XX	PS	for detecting presence of prostate cancer, stage of prostate cancer -	
XX		Claim 1; Page 6204-6205; 11750BP; English.	

Claim 1; Page 6204-6205; 11750pp; English

QY	1871	CGGCAAGTGTGGAGGAGGAGGGGTGGAGGCTCCCAATTTGAGATCTCTGCTGAGTCC	1930
Db	1932	CGGTCAAGTGTGAGGAGGAGGGGTGGAGGCTCCCAATTTGAGATCTCTCTGAGTCT	1991
QY	1931	TTTCCAGGGGCCAATTTTGGATGAGCAATGAGAGCTGTACCTCTCAGACTCTGGATGACTTG	1990
Db	1992	TTTCCAGGGGCCAATTTTGGATGAGCAATGAGAGCTGTACCTCTCAGACTCTGGATGACTTG	2051
QY	1991	AGATGAAAAAGAGAGACATGGAAAGGAGACAGCCAGGTGGACCTGCAGCGGCTG-CC	2049
Db	2052	AGATGAAAAAGAGAGACATGGAAAGGAGAGACAGCCAGGTGGACCTGCAGCGGCTGCC	2111
QY	2050	TTCTGGGGGCCACTTGTGATGTCTCCCAAGCCCTACTCTCCACAAGGGGATTTTGTGATGAGG	2109
Db	2112	TTCTGGGGGCCACTTGTGATGTCTCCCAAGCCCTACTCTCCACAAGGGGATTTTGTGATGAGG	2171
QY	2110	TTTCTTAAAGCCTTAAAGAGCCCTGGATGATGGGCGCAGAAATTAAGGGAGACGCCCTTCAATG	2169
Db	2172	TTTCTTAAAGCCTTAAAGAGCCCTGGATGATGGGCGCAGAAATTAAGGGAGACGCCCTTCAATG	2231
QY	2170	GTGGTGACGTGTGATGATCTGTAAAGGGGAAACAGAAACATTTTGTCTTATGGGTGA	2229
Db	2232	GTGGTGACGTGTGATGATCTGTAAAGGGGAAACAGAAACATTTTGTCTTATGGGTGA	2290
QY	2230	GAAATATGAAAGTCCCTTTGGGTGGGCGAAGGAAAGCAATTTGAAAGAACTTGTGCCCTGAGCA	2289
Db	2291	GAAATATGAAAGTCCCTTTGGGTGGGCGAAGGAAAGCAATTTGAAAGAACTTGTGCCCTGAGCA	2349
QY	2290	CTTCTGGTGGAGGCTGCTCAGCTCACAATTTGGGTGGGCGCTCCGGAGGGAGAGCTCAGGCT	2349
Db	2350	CTTCTGGTGGAGGCTCCTCAGCTCACAATTTGGGTGGGCGCTCCGGAGGGAGAGCTCAGGCT	2409
QY	2350	TTCTCTCATCTCTCCCTGAGCCCTGCTCTAGCACCCCTGAGAGTGCACATGCCCTTGTGT	2409
Db	2410	TTCTCTCATCTCTCCCTGAGCCCTGCTCTAGCACCCCTGAGAGTGCACATGCCCTTGTGT	2469
QY	2410	CTTGGGCGAGGGGCGCCAAAGTGTGGACCACTGTTTGGCTCTTACGCCCTGTGATGACTGG	2469
Db	2470	CTTGGGCGAGGGGCGCCAAAGTGTGGACCACTGTTTGGCTCTTACGCCCTGTGATGACTGG	2527
QY	2470	AAATTTGAGTGCATAGGGGGGAAATCAAGAGATGCTCAGTTTAAAGTCACTGTTTCCATGTT	2529
Db	2538	AAATTTGAGTGCATAGGGGGGAAATCAAGAGATGCTCAGTTTAAAGTCACTGTTTCCATGTT	2587
QY	2530	ATGTTTCTACACATTTGCTACTCTAGTCTCTGCGAAACCTTACTTTGATGTCTCCAAGT	2589
Db	2588	ATGTTTCTACACATTTGCTACTCTAGTCTCTGCGAAACCTTACTTTGATGTCTCCAAGT	2647
QY	2590	AGTCCACCTTCAATTTAACTCTTTTGAATGTAATCATCTTGTGCCAAGTAAGAGTGTGGCC	2649
Db	2648	AGTCCACCTTCAATTTAACTCTTTTGAATGTAATCATCTTGTGCCAAGTAAGAGTGTGGCC	2707
QY	2650	TATTTTCAAGTGTGTTTGAACAAATGACTGGCTCTGACTTAAAGTTCCTTAAATGAATGTG	2709
Db	2708	TATTTTCAAGTGTGTTTGAACAAATGACTGGCTCTGACTTAAAGTTCCTTAAATGAATGTG	2767
QY	2710	CTGAGAGCAAAAGTCCCATGGTGGCGCGCGAAGAAAGAAAGATGTGTTTGTGTTTGGACTC	2769
Db	2768	CTGAGAGCAAAAGTCCCATGGTGGCGCGCGAAGAAAGAAAGATGTGTTTGTGTTTGGACTC	2827
QY	2770	TTCTGTGTCCCTTCCAAATGCTGTGGGTTCCAACCAAGGGGAAAGGCTCCCTTTTGCATTC	2829
Db	2828	TTCTGTGTCCCTTCCAAATGCTGTGGGTTCCAACCAAGGGGAAAGGCTCCCTTTTGCATTC	2887
QY	2830	CAATGTCCATTAACCATGAGACATCTACATGTTTCTGCTCTGTGGCCAAAGAGGCTG	2889
Db	2888	CAATGTCCATTAACCATGAGACATCTACATGTTTCTGCTCTGTGGCCAAAGAGGCTG	2947
QY	2890	GTTTGGCAAGATGAATGAATGATTTCTTACAGTATGAGACTTAACTGTAAGATGAGAAAGTCT	2949
Db	2948	GTTTGGCAAGATGAATGAATGATTTCTTACAGTATGAGACTTAACTGTAAGATGAGAAAGTCT	3007

OY	2950	TGCATCCCAATTTGACAGATCCGCTGCTGACATGCTGTAGAGAGACGATTTCCAG	3009
Db	3008	TGCAATCCCAATTTGACAGATCCGCTGCTGACATGCTGTAGAGAGACGATTTCCAG	3067
OY	3010	GGACCTTGGAAACAGTTGGCAGCTGAAGTGCTGTGCTCCCAAGACACATCCTAAAGT	3069
Db	3068	GGACCTTGGAAACAGTTGGCAGCTGAAGTGCTGTGCTCCCAAGACACATCCTAAAGT	3127
OY	3070	GTTCTATGGGAAACGCTGCTCCTTATTTGCCCTTCTATTTATGTGAACAATCG	3129
Db	3128	GTTCTATGGGAAACGCTGCTCCTTATTTATTTATTTATTTATGTGAACAATCG	3187
OY	3130	TTTCTCTTTTGTATCTTTTAAACGTAAAGTTCAATGTGAATAATGATATCAATG	3189
Db	3188	TTTCTCTTTTGTATCTTTTAAACGTAAAGTTCAATGTGAATAATGATATCAATG	3247
OY	3190	CAATTAATTTATGCGATTTTTTTTCAAGTAACACGCTGATCTTTGAAGTTCTGCTGG	3249
Db	3248	CAATTAATTTATGCGATTTTTTTTCAAGTAACACGCTGATCTTTGAAGTTCTGCTGCG	3307
OY	3250	TGATAGGACAGCGCTCACTTTCTTATAAGGGGGGATGTTGAGGCTGCTGGCAGAGG	3309
Db	3308	TGATAGGACAGCGCTCACTTTCTTATAAGGGGGGATGTTGAGGCTGCTGGCAGAGG	3367
OY	3310	ACCAAGGTGAGCGACGACGACACTTGGTCTCTGTGGTGGTGGCTGCACTGCTTCCGCA	3369
Db	3368	ACCAAGGTGAGCGACGACGACACTTGGTGGTCTCTGTGGTGGTGGCTGCACTGCTTCCGCA	3426
OY	3370	GCGCTGCTGTGGAGGTCCTCAAAAGTCCCTTATTTATTTATTTATTTATGCTGTG	3426
Db	3427	GCGCTGCTGTGGAGGTCCTCAAAAGTCCCTTATTTATTTATTTATTTATGCTGTG	3483

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RESULT 10
AAC83325
ID AAC83325 standard; DNA; 3966 BP.
XX
XX AAC83325;
AC
XX 26-FEB-2001 (first entry)
DT
XX Human TMPRSS2 DNA.
DE
XX
XX Prostate specific androgen regulated protein; ARSDRL; TMPRSS2;
KW PART-1; neoplastic; ds.
XX
XX Homo sapiens.
OS
XX
XX W0200065067-A2.
XX
XX
XX 02-NOV-2000.
PD
XX
XX
XX 21-APR-2000; 2000MO-US10920.
PF
XX
XX 23-APR-1999; 99US-0130778.
PR 30-AUG-1999; 99US-0151585.
PR 30-DEC-1999; 99US-0174003.
PR 24-JAN-2000; 2000US-0177751.
XX
XX (UNIM ) UNIV WASHINGTON.
PA
XX
XX Nelson PS, Hood L, Lin B;
PI
XX
XX WPI: 2000-679676/56.
DR P-PSDB; AAB36901.
XX
XX Polynucleotide encoding prostate specific androgen regulated
PT polypeptides and inhibitor of the peptides useful for treating or
PT reducing the progression of prostate neoplastic condition in an
PT individual -
XX
XX Claim 1; Page 81-86; 121pp; English.
XX

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CC The present invention relates to prostate specific androgen regulated
CC proteins. The invention may be used to determine an expression level
CC of the prostate-specific proteins ARSD1, TMPRSS2, or PAB1 in a
CC fluid sample or prostate cell sample from an individual. It may also
CC be used for diagnosing and predicting the susceptibility of a
CC prostate neoplastic condition in an individual. Inhibitors of the
CC proteins are useful for treating or preventing the progression of a
CC prostate neoplastic condition.

XX Sequence 3966 BP; 992 A; 998 C; 988 G; 984 T; 4 other;

Query Match 94.0%; Score 3236.6; DB 21; Length 3966;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3324; Conservative 4; Mismatches 18; Indels 9; Gaps 7;

QY 93 GTCAATTTGAACATTCAGATACATATCATGATGCTGTTGATATACAGCAAGATGG 152
DB 1 GTCAATTTGAACATTCAGATACATATCATGATGCTGTTGATATACAGCAAGATGG 60
QY 153 CTTTGAACATTCAGATACATTCAGATACATTCAGATACATTCAGATACATTCAGATAC 212
DB 61 CTTTGAACATTCAGATACATTCAGATACATTCAGATACATTCAGATACATTCAGATAC 120
QY 213 CGGAAACCCCTATCCGACAGCCACTGTGTCCACTGTCTAGAGGTGATCCGG 272
DB 121 CGGAAACCCCTATCCGACAGCCACTGTGTCCACTGTCTAGAGGTGATCCGG 180
QY 273 CTGAGTACTACCCGTCGCCCGCCAGTACGAGCCGAGGCTCCTGACGAGGCTTCCA 332
DB 181 CTGAGTACTACCCGTCGCCCGCCAGTACGAGCCGAGGCTCCTGACGAGGCTTCCA 240
QY 333 ACCCGCTGCTGACAGCAGCCCAATCCCATCCGAGACAGTGTGACCTCAAGACTA 392
DB 241 ACCCGCTGCTGACAGCAGCCCAATCCCATCCGAGACAGTGTGACCTCAAGACTA 300
QY 393 AGAAGACATGTGATACCTTGAACCTTGGGAGCTTCTGTGGAGCTGCTGGCG 452
DB 301 AGAAGACATGTGATACCTTGAACCTTGGGAGCTTCTGTGGAGCTGCTGGCG 360
QY 453 CTGAGTACTACCCGTCGCCCGCCAGTACGAGCCGAGGCTCCTGACGAGGCTTCCA 512
DB 361 CTGAGTACTACCCGTCGCCCGCCAGTACGAGCCGAGGCTCCTGACGAGGCTTCCA 420
QY 513 CTTGAGTACTACCCGTCGCCCGCCAGTACGAGCCGAGGCTCCTGACGAGGCTTCCA 572
DB 421 CTTGAGTACTACCCGTCGCCCGCCAGTACGAGCCGAGGCTCCTGACGAGGCTTCCA 480
QY 573 GGGAGGAGCAATTCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 632
DB 481 GGGAGGAGCAATTCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 540
QY 633 CATCTCAGAGGAGTCTGTCGACCTGTGTGCTGTCAGAGAGTGTGAGAGTGTGAGG 692
DB 541 CATCTCAGAGGAGTCTGTCGACCTGTGTGCTGTCAGAGAGTGTGAGAGTGTGAGG 600
QY 693 GGGGCGCTGACAGGAGATGGGCTATGAAGAAATTTTACTAGCCAGGAATAGTGG 752
DB 601 GGGGCGCTGACAGGAGATGGGCTATGAAGAAATTTTACTAGCCAGGAATAGTGG 660
QY 753 ATGACAGGAGTTCACCAAGCTTTATGAACCTGAAACAGAGTGTGCTGATCT 812
DB 661 ATGACAGGAGTTCACCAAGCTTTATGAACCTGAAACAGAGTGTGCTGATCT 720
QY 813 ATAAAAAATCTACACAGTATGCTGTTCTTCAAAAAGAGTGTGTTCTTACGCTGTA 872
DB 721 ATAAAAAATCTACACAGTATGCTGTTCTTCAAAAAGAGTGTGTTCTTACGCTGTT 780
QY 873 TAGCCTCGGGGCTCACTTGAAGTCAAGCCGACAGAGAGATGCTGGCGCGAGAGCG 932
DB 781 TAGCCTCGGGGCTCACTTGAAGTCAAGCCGACAGAGAGATGCTGGCGCGTGAAGCG 840
QY 933 CGCTCCCGGGGCTGCGCTGGGAGGTCAAGCTGACAGTCAAGAGTCCACGCTGTCG 992

DB 841 CGCTCCCGGGGCTGCGCTGGGAGGTCAAGCTGACAGTCAAGAGTCCACGCTGTCG 899
QY 993 GGAGGCTCATCATCAACCCGAGAGTGTGATGAGAGCGGCGCCACTGGTGGAAAAACT 1052
DB 900 GGAGGCTCATCATCAACCCGAGAGTGTGATGAGAGCGGCGCCACTGGTGGAAAAACT 959
QY 1053 CTTAAACATTCAGATGACGATGACGATGACGATGACGATGACGATGACGATGACGATG 1112
DB 960 CTTAAACATTCAGATGACGATGACGATGACGATGACGATGACGATGACGATGACGATG 1019
QY 1113 TATGAGCCGAGATACCAAGTGAAGAAAGTATTTCTATCCAAATTTAGTCCAGACC 1172
DB 1020 TATGAGCCGAGATACCAAGTGAAGAAAGTATTTCTATCCAAATTTAGTCCAGACC 1079
QY 1173 AAGAAATGACATTTGGCTGATGAGAGTGAAGAGCTGATGATGATGATGATGATGATG 1232
DB 1080 AAGAAATGACATTTGGCTGATGAGAGTGAAGAGCTGATGATGATGATGATGATGATG 1139
QY 1233 AAACAGTGTGTCTGCCCAACCCAGGAGTGTGATGATGATGATGATGATGATGATGATG 1292
DB 1140 AAACAGTGTGTCTGCCCAACCCAGGAGTGTGATGATGATGATGATGATGATGATGATG 1199
QY 1293 TCCGGGTGGGGGCGCCAGAGAGAAAGGAAAGCTCTGAGAGTGTGATGATGATGATG 1352
DB 1200 TCCGGGTGGGGGCGCCAGAGAGAAAGGAAAGCTCTGAGAGTGTGATGATGATGATG 1259
QY 1353 GTGCTTCATTTGAGACAGAGATGCAAGAGATGATGATGATGATGATGATGATGATG 1412
DB 1260 GTGCTTCATTTGAGACAGAGATGCAAGAGATGATGATGATGATGATGATGATGATG 1319
QY 1413 CCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1472
DB 1320 CCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1379
QY 1473 GGAGGCTCTGTGTGATCTTGAAGAAAGTATGATGATGATGATGATGATGATGATGATG 1532
DB 1380 GGAGGCTCTGTGTGATCTTGAAGAAAGTATGATGATGATGATGATGATGATGATGATG 1439
QY 1533 GATTCGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1592
DB 1440 GATTCGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1499
QY 1593 GACTGATTTATCGCAAAATGAGGAGAGGCTATATCATGATGATGATGATGATGATGATG 1652
DB 1500 GACTGATTTATCGCAAAATGAGGAGAGGCTATATCATGATGATGATGATGATGATGATG 1559
QY 1653 TCGTTTTCAGAAAGAAAGTGGGCTGTTGCTGCTCCCGTGCATGATTTACTTGA 1712
DB 1560 TCGTTTTCAGAAAGAAAGTGGGCTGTTGCTGCTCCCGTGCATGATTTACTTGA 1619
QY 1713 GATGATTCAGAGTCACTTCAATTTTATTAACAGTAACTGTGCTTGGCACTCT 1772
DB 1620 GATGATTCAGAGTCACTTCAATTTTATTAACAGTAACTGTGCTTGGCACTCT 1679
QY 1773 CTGCCATTCGTGCAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1832
DB 1680 CTGCCATTCGTGCAAGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1739
QY 1833 TCCGCAAGGGTGTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1890
DB 1740 TCCGCAAGGGTGTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1799
QY 1891 GGGTGGAGGCTG-CGCCATTTAGATCTTCTGCTGAGTCTTCTTCAAGGGGCAATTTGG 1949
DB 1800 GGGTGGAGGCTGCCCCCATTTAGATCTTCTGCTGAGTCTTCTTCAAGGGGCAATTTGG 1859
QY 1950 ATGACATGAGAGTGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2009
DB 1860 ATGACATGAGAGTGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1919
QY 2010 TGGAAAGGAGACAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2068
DB 1920 TGGAAAGGAGACAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1979

QY	2069	GTCCCCAGCCTACTCTCCACAAAGGGGATTTTGCGATGGGCTTTAAAGCCTTAGACAGC	21288
Db	1980	GTCCCCAGCCTACTCTCCACAAAGGGGATTTTGCGATGGGCTTTAAAGCCTTAGACAGC	20399
QY	2129	CTTGGAATGCTGGCCAGAAATAAAGGAGCAGCCCTTCATGGGTGGTACGTGTAGTCAC	21888
Db	2040	CTTGGAATGCTGGCCAGAAATAAAGGAGCAGCCCTTCATGGGTGGTACGTGTAGTCAC	20988
QY	2189	CTTTGTAAGGGGAAACAGAAACATTTTGTCTTATATGGGGGAGAAATATAGACAGTGCCTT	22488
Db	2099	CTTTGTAAGGGGAAACAGAAACATTTTGTCTTATATGGGGGAGAAATATAGACAGTGCCTT	21588
QY	2249	GGGTGCGAGGGAAGCAATTTGAAAAAGAACCTTGCCCTGAGCACCTCTGTGTGACGTCTTCCA	23088
Db	2159	-GGTGCAGAGGAAGCAATTTGAAAAAGAACCTTGCCCTGAGCACCTCTGTGTGACGTCTTCCA	22177
QY	2309	CTTGACATTTGGGTGGGGGCTCTGGGAGGGAGATCAGCTTCTCTCTCATCTCTCTGGA	23688
Db	2218	CTTGACATTTGGGTGGGGGCTCTGGGAGGGAGATCAGCTTCTCTCTCATCTCTCTGGA	22777
QY	2369	CCCTGCTCTCAGACACCTGTGAGAGTGCACATGCCCCCTTGCTCTGTGGGAGGGGGCCCAAG	24288
Db	2278	CCCTGCTCTCAGACACCTGTGAGAGTGCACATGCCCCCTTGCTCTGTGGGAGGGGGCCCAAG	23355
QY	2429	TCGTGGACCATGTTGGCCTTCTCAGGCGCTGTAGTCACTGTGAATTTGAGTCATGAGGGG	24888
Db	2336	TCGTGGACCATGTTGGCCTTCTCAGGCGCTGTAGTCACTGTGAATTTGAGTCATGAGGGG	23955
QY	2489	AAATTCAGAGTATGCTCAGTTTAAGAGTACACTGTTTCCATGTTATGTTCTTACACATGTGTA	25488
Db	2396	AAATTCAGAGTATGCTCAGTTTAAGAGTACACTGTTTCCATGTTATGTTCTTACACATGTGTA	24555
QY	2549	CCCTCAGTGTCTCTGGAACCTTAAGCTTTTGATGTCTCCAGTATGTCACACTTCATTTAACT	26088
Db	2456	CCCTCAGTGTCTCTGGAACCTTAAGCTTTTGATGTCTCCAGTATGTCACACTTCATTTAACT	25155
QY	2609	CTTTGGAACCTGTATCATCTTTTGGCAGTAAAGTGTGTGGCCATTTTCAGCTGTCTTGACA	26688
Db	2516	CTTTGGAACCTGTATCATCTTTTGGCAGTAAAGTGTGTGGCCATTTTCAGCTGTCTTGACA	25755
QY	2669	AAATGATGTGCTCTCTGACTTAAAGCTTCTAATTAATGATGTGTGAAGCAAAAGTGGCCATG	27288
Db	2576	AAATGATGTGCTCTCTGACTTAAAGCTTCTAATTAATGATGTGTGAAGCAAAAGTGGCCATG	26355
QY	2729	GTGGCGGCGGAAGAAAGATGTGTTTTGTTTGGACTCTGTGTGCTCCCTTCATAG	27888
Db	2636	GTGGCGGCGGAAGAAAGATGTGTTTTGTTTGGACTCTGTGTGCTCCCTTCATAG	26955
QY	2789	CTGTGGGTTTCCAAACAGGGGGAAGGGTCCCTTGTGATGGCCAAATGCGATTAACCATAG	28488
Db	2696	CTGTGGGTTTCCAAACAGGGGGAAGGGTCCCTTGTGATGGCCAAATGCGATTAACCATAG	27555
QY	2849	CATTAACCTACATGATGTGTGCTCTCTGTGGCCAAAGAGGTGTGTTTGGCAAGATGAATAGA	29088
Db	2756	CATTAACCTACATGATGTGTGCTCTCTGTGGCCAAAGAGGTGTGTTTGGCAAGATGAATAGA	28155
QY	2909	ATGATTTCTAAGCTAGACATTTAACTTTGAATGGAAGCTTTTGCACATCCCATTTGACAGA	29688
Db	2816	ATGATTTCTAAGCTAGACATTTAACTTTGAATGGAAGCTTTTGCACATCCCATTTGACAGA	28755
QY	2969	TCCCTGTGTGCACATGCTCTGTGAGAGACAGATCCCAAGGACCTTGGAAACAGTTGG	30288
Db	2876	TCCCTGTGTGCACATGCTCTGTGAGAGACAGATCCCAAGGACCTTGGAAACAGTTGG	29355
QY	3029	CACGTATAGGTGCTGTGCTCCCAAGACACATCCTTAAAGGTTGTAAATGCTGAAGAACGT	30888
Db	2936	CACGTATAGGTGCTGTGCTCCCAAGACACATCCTTAAAGGTTGTAAATGCTGAAGAACGT	29955
QY	3089	CTTCCCTTTTAATGGCCCCCTTCTAATTTATATATGGAACAACATGTTGTGCTTTTGTATCT	31488
Db	2996	CTTCCCTTTTAATGGCCCCCTTCTAATTTATATATGGAACAACATGTTGTGCTTTTGTATCT	30555

OY	14	CGGTAGGGCCGAGACTTAAGCAGAGAGGGGAGAGGGGAGAGGGGCGAGGGGCGAGGGGCGGAGGC	73
Dd	10	CGCGTCGGCGGACCTTAAGCAGAGAGGGGAGGGGAGGGGCGAGGGGCGAGGGGCGGAGGC	69
OY	74	GCCCGCTGGAGCCCGGCGAGGCTCATATTGAAACATTCACAGTACTTATCATTACTCATCT	133
Dd	70	GCCCGCTGGAGCCCGGCGAGGCTCATATTGAAACATTCACAGTACTTATCATTACTCATCT	129
OY	134	GTTGATTAACAGCAAGATGGCTTTTGAACTCAGGGGTCACACAGCCTATTGGACCTTACTAT	193
Dd	130	GTTGATTAACAGCAAGATGGCTTTTGAACTCAGGGGTCACACAGCCTATTGGACCTTACTAT	189
OY	194	GAATAACCATGGATATCCAAACCGGGAAAAACCCCTATCCCGGACACCCACACCTGTGGTCCCCACT	253
Dd	190	GAATAACCATGGATATCCAAACCGGGAAAAACCCCTATCCCGGACACCCACACCTGTGGTCCCCACT	249
OY	254	GTTCTACGAGGTGATPCCGCGCTCAGTACTACCCGTCCCGGTCGCCAGNACCCCGGAGG	313
Dd	250	GTTCTACGAGGTGATPCCGCGCTCAGTACTACCCGTCCCGGTCGCCAGNACCCCGGAGG	309
OY	314	GTCCTGACGCGAGGCTTCCAAACCCCGTGTCTGTCAGCGACGACCCCAATTCCCATTCGGGACA	373
Dd	310	GTCCTGACGCGAGGCTTCCAAACCCCGTGTCTGTCAGCGACGACCCCAATTCCCATTCGGGACA	369
OY	374	GTTGTGACACCTTCAAGACTATAAGAAAGCAGTGTGATACCTTGACCTTGGGAGACTTCTCTC	433
Dd	370	GTTGTGACACCTTCAAGACTATAAGAAAGCAGTGTGATACCTTGACCTTGGGAGACTTCTCTC	429
OY	434	GTTGGAGCTGGCGTGGCGCGCTGAGCTTACTGTGAAATTATGGGAGCAAGTGCCTCCAC	493
Dd	430	GTTGGAGCTGGCGTGGCGCGCTGAGCTTACTGTGAAATTATGGGAGCAAGTGCCTCCAC	489
OY	494	TCTGGGATAGAGTGCAGCTCTCAGGTACCTGTCATCAACCCCTTAACTGTGTGTATGGC	553
Dd	490	TCTGGGATAGAGTGCAGCTCTCAGGTACCTGTCATCAACCCCTTAACTGTGTGTATGGC	549
OY	554	GTTGTACACACTTCCCCCGGGCGGGGAGAGACAGAAATCGGTGTGTTCGCTCTAGGAGCCAAAC	613
Dd	550	GTTGTACACACTTCCCCCGGGCGGGGAGAGAAATCGGTGTGTTCGCTCTAGGAGCCAAAC	609
OY	614	TTTCACTCTTACGAGTGTACTCATCTCAGAGAGAAATCCTGTGCACCTGTGTGGCCAAACAGAC	673
Dd	610	TTTCACTCTTACGAGTGTACTCATCTCAGAGAGAAATCCTGTGCACCTGTGTGGCCAAACAGAC	669
OY	674	TGGAACGAGAACTACGGGCGGGCGGGCCTGCAGGGACATGGGCTATTAAGATTAATTTTAC	733
Dd	670	TGGAACGAGAACTACGGGCGGGCGGGCCTGCAGGGACATGGGCTATTAAGATTAATTTTAC	729
OY	734	TCTTAGCCAAAGAAATAGTGTGATGACAGCGGATCCACACGTTTATGAACTGAAACAAGT	793
Dd	730	TCTTAGCCAAAGAAATAGTGTGATGACAGCGGATCCACACGTTTATGAACTGAAACAAGT	789
OY	794	GCCGCGAATGTGCAATATCTATTAAAAAACTTACCAAGATGATGCCGTTCTTCAAAAGCA	853
Dd	790	GCCGCGAATGTGCAATATCTATTAAAAAACTTACCAAGATGATGCCGTTCTTCAAAAGCA	849
OY	854	GTTGTTTCTTACGCTGTATAGCCTGCGGGGGTCAACTTGAACCTCAAGCGCCAGCAGCAGG	913
Dd	850	GTTGTTTCTTACGCTGTATAGCCTGCGGGGGTCAACTTGAACCTCAAGCGCCAGCAGCAGG	909
OY	914	ATTCGTGGGCGGCGAGACGCGCTTCCGGGGGGCTGGCCCTGGGCGAGTCAAGCTCAGCT	973
Dd	910	ATTCGTGGGCGGCGAGACGCGCTTCCGGGGGGCTGGCCCT - GGACAGTTCAGCCTCAGCT	968
OY	974	CCAGAAGTCCACGTGTGGGAGGCTCANTCANTCACACCCCGAGTGGATGTGACAGCCGC	1033
Dd	969	CCAGAAGTCCACGTGTGGGAGGCTCANTCANTCACACCCCGAGTGGATGTGACAGCCGC	1028
OY	1034	CCAGTGGCTGGAAAAACCTTTAAACATCATGGCATTTGGAGCGGCAATTTTGGCGGATTTT	1093
Dd	1029	CCAGTGGCTGGAAAAACCTTTTAAACAATCATGGCATTTGGAGCGGCAATTTTGGCGGATTTT	1088
OY	1094	GAGACAACTTTCATGTCTTATGTAGAGCGGATACCAAGTAGAAAAAGTATTTTCATACC	1153

[illegible]


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Db 2169 GTGACGTGGTAGTCA-CTTTGTAAGGGGAACAGAAACATTTTGTCTTATGGGTAGAA 2227
Oy 2233 TATAGACATGGCCCTTGGGTGGGAGGGAAGCAATTTGAAAAAGAACTTGGCCGTAGCATC 2292
Db 2228 TATAGACATGGCCCTT-GGTGGAGGGAAGCAATTTGAAAAAGAACTTGGCCGTAGCATC 2286
Oy 2293 CTGGTGCAGGTCTCCACCTGCACATTTGGGTGGGGCTCTGGAGGAGAGACTAGCCTTCC 2352
Db 2287 CTGGTGCAGGTCTCCACCTGCACATTTGGGTGGGGCTCTGGAGGAGAGACTAGCCTTCC 2346
Oy 2353 TCCCTATCTCCCTGCACCTGTCTCCAGAACCCCTGGAGAGTGCACATGGCCCTTGGCTCT 2412
Db 2347 TCCCTATCTCCCTGCACCTGTCTCCAGAACCCCTGGAGAGTGCACATGGCCCTTGGCTCT 2406
Oy 2413 GGGAGGGGGCGCAAGTCTGGCACATGTGGCCCTTTCAGGCGCTCTAGTCACTGGAAA 2472
Db 2407 GG--CAGGGCGGCAAGTCTGGCACATGTGGCCCTTTCAGGCGCTCTAGTCACTGGAAA 2464
Oy 2473 TTGAGTCCATGGGGGAAATCAAGATGCTCAAGTTTAAAGTACATGTTTCCATGTTTATG 2532
Db 2465 TTGAGTCCATGGGGGAAATCAAGATGCTCAAGTTTAAAGTACATGTTTCCATGTTTATG 2524
Oy 2533 TTTCTACATGCTACCTACGTCAGTGCCTGGAAAGTCTTGTGATGTCCTCCAGTAGT 2592
Db 2525 TTTCTACATGCTACCTACGTCAGTGCCTGGAAAGTCTTGTGATGTCCTCCAGTAGT 2584
Oy 2593 CCACCTTCATTTAACTCTTGAAGTATCATCTTGGCAATAGAGTGTGGCCTAT 2652
Db 2585 CCACCTTCATTTAACTCTTGAAGTATCATCTTGGCAATAGAGTGTGGCCTAT 2644
Oy 2653 TTTACGCTGTTTGAACAAATGACGTGCTCCTGCATTAAAGTCTTAAATGAATGTGCTG 2712
Db 2645 TTTACGCTGTTTGAACAAATGACGTGCTCCTGCATTAAAGTCTTAAATGAATGTGCTG 2704
Oy 2713 AAGCAAGGCCCATGGTGGGGGGAAGAAAGATGTTTGTGTTTGGACCTCTC 2772
Db 2705 AAGCAAGGCCCATGGTGGGGGGAAGAAAGATGTTTGTGTTTGGACCTCTC 2764
Oy 2773 GTGGTCCCTTCCAAATGCTGTGGGTTCCAAACAGGGGAAGGGTCCCTTGTGCTGCA 2832
Db 2765 GTGGTCCCTTCCAAATGCTGTGGGTTCCAAACAGGGGAAGGGTCCCTTGTGCTGCA 2824
Oy 2833 GTGGCATAACCATGACACTACTCTAACCATGTTTGTGCTGCTGCGCAAGCAGGCTGTT 2892
Db 2825 GTGGCATAACCATGACACTACTCTAACCATGTTTGTGCTGCTGCGCAAGCAGGCTGTT 2884
Oy 2893 TGCAGAAATGAATGAATGATTTCTACAGTAGAGACTTAACCTTGAATGGAATGCTTGC 2952
Db 2885 TGCAGAAATGAATGAATGATTTCTACAGTAGAGACTTAACCTTGAATGGAATGCTTGC 2944
Oy 2953 AATCCATTTGACGATCCGCTGTGTCACATGCTCTGTAGAGAGAGATTTCCAGGGA 3012
Db 2945 AATCCATTTGACGATCCGCTGTGTCACATGCTCTGTAGAGAGAGATTTCCAGGGA 3004
Oy 3013 CCTTGGAAACAGTTGGCACTGTAAAGTGTGCTGCCCAAGACACATCTTAAAAAGTGT 3072
Db 3005 CCTTGGAAACAGTTGGCACTGTAAAGTGTGCTGCCCAAGACACATCTTAAAAAGTGT 3064
Oy 3073 GTRATGTTGAAAAAGCTCTCTCTTATTTGCCCCCTTCTTATTTATGTGAACAAGTGT 3132
Db 3065 GTRATGTTGAAAAAGCTCTCTCTTATTTGCCCCCTTCTTATTTATGTGAACAAGTGT 3124
Oy 3133 GTCTTTTGTGTTTCTTTTAACTGTAAGTTCAATTTGTAATGTAATATCATGCA 3192
Db 3125 GTCTTTTGTGTTTCTTTTAACTGTAAGTTCAATTTGTAATGTAATATCATGCA 3184
Oy 3193 ATTAATTTATGCGATTTTCTTTTCAAGTAA 3222
Db 3185 ATTAATTTATGCGATTTTCTTTTCAAGTAA 3214

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RESULT 13
AAH93942

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ID AAH93942 standard; cDNA; 3245 BP.
XX
AC AAH93942;
XX
DT 04-OCT-2001 (first entry)
XX
DE P100C full length cDNA sequence.
XX
KW Human: prostate cancer; prostate-specific; diagnosis; vaccine;
  cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (COR-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;
PI Wang A, Meagher MJ;
XX
DR MPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; page 537-538; 543pp: English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AA01115 to
CC AA01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 3245 BP; 774 A; 818 C; 870 G; 783 T; 0 other;
XX
Query Match 91.1%; Score 3136.8; DB 22; Length 3245;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3197; Conservative 0; Mismatches 7; Indels 6; Gaps 5;
Oy 14 CGAGTGGCGCGGAGCTAAGCAGAGGCGGAGGGGAGGCGGAGGGGGAGC 73
Db 10 GCGGTCCGCGGAGCTAAGCAGAGGCGGAGGGGAGGCGGAGGGCGAGG 69
Oy 74 GCGGCTGGAGCGCGGAGGCTATTTGAACATTTCCAGATTCATCTACTGATGCT 133
Db 70 GCGGCTGGAGCGCGGAGGCTATTTGAACATTTCCAGATTCATCTACTGATGCT 129
Oy 134 GTTGATTAACGCAAGATGCTTTGAAGTCAAGGTCACACAGCTATTTGACCTTACTAT 193
Db 130 GTTGATTAACGCAAGATGCTTTGAAGTCAAGGTCACACAGCTATTTGACCTTACTAT 189
Oy 194 GAATACCATGATTAACCAAGCGAAACCCCTATTCGCGCAAGCGCCAGTGGTCCCACT 253
Db 190 GAATACCATGATTAACCAAGCGAAACCCCTATTCGCGCAAGCGCCAGTGGTCCCACT 249
Oy 254 GTCTAGAGGTGATCCGCGCTCAGTACTACCGTCCCGCTGCGCCAGTACGCCCGAGG 313

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Db 250 GTCTACGAGGTGCATCCGGCTGTAGTACACCGTCCCGGCTGCCAGTACGCCCGAGG 309
OY 314 GTCTGACGACGAGGCTTCCAAACCCGCTGCTGTACGACGAGCCCAATCCCATCCGGAGCA 373
Db 310 GTCTGACGACGAGGCTTCCAAACCCGCTGCTGTACGACGAGCCCAATCCCATCCGGAGCA 369
OY 374 GTGTGACCTCCCAAGAGCTAGAAAGCACTGTGTCATACCTTGACCTGGGGACCTTCTC 433
Db 370 GTGTGACCTCCCAAGAGCTAGAAAGCACTGTGTCATACCTTGACCTGGGGACCTTCTC 429
OY 434 GTGGAGGTGGGCTGGGCTGGGCTGTCTGTGGAAGTTCATGAGGAGCAAGTGTCCAAAC 493
Db 430 GTGGAGGTGGGCTGGGCTGGGCTGTCTGTGGAAGTTCATGAGGAGCAAGTGTCCAAAC 489
OY 494 TCTGGGATAGAGTGGGCTGTCTGTGGAAGTTCATGAGGAGCAAGTGTCCAAAC 553
Db 490 TCTGGGATAGAGTGGGCTGTCTGTGGAAGTTCATGAGGAGCAAGTGTCCAAAC 549
OY 554 GTGTGACACTGCCCCGGGGGGGAGGAGCAAGATCGGTGTTCGCTGTACGGACCAAC 613
Db 550 GTGTGACACTGCCCCGGGGGGGAGGAGCAAGATCGGTGTTCGCTGTACGGATCAAC 609
OY 614 TTCACTCTTACGCTGTCTGTGGAAGTTCATGAGGAGCAAGTGTCCAAAC 673
Db 610 TTCACTCTTACGCTGTCTGTGGAAGTTCATGAGGAGCAAGTGTCCAAAC 669
OY 674 TGGAGAGAGATACGAGGCGGGGCTGTGACGAGCATGGGCTATAGAAATATTTTAC 733
Db 670 TGGAGAGAGATACGAGGCGGGGCTGTGACGAGCATGGGCTATAGAAATATTTTAC 729
OY 734 TCTTACCAAGAGATAGTGTGTACAGCGGATCCACAGCTTTATGAACTGAACACAGT 793
Db 730 TCTTACCAAGAGATAGTGTGTACAGCGGATCCACAGCTTTATGAACTGAACACAGT 789
OY 794 GCCGCAATGTGATGTATATAAAAGCTTACACAGTATGATGCTTCTCAAAAGCA 853
Db 790 GCCGCAATGTGATGTATATAAAAGCTTACACAGTATGATGCTTCTCAAAAGCA 849
OY 854 GTGGTTCTTTTACGCTGTATAGCTGTGCGGGGTCAACTTGAACCTCAAGCCGACAGCAG 913
Db 850 GTGGTTCTTTTACGCTGTATAGCTGTGCGGGGTCAACTTGAACCTCAAGCCGACAGCAG 909
OY 914 ATCTGGGGGCGGAGAGCGGCTCCCGGGGGCTTGCGGCTGGGCAAGTGCCTGCAGT 973
Db 910 ATCTGGGGGCGGAGAGCGGCTCCCGGGGGCTTGCGGCTGGGCAAGTGCCTGCAGT 968
OY 974 CCAGAAAGCTCCAGTGTGGGAGGCTCATCATCAACCCCGAGTGTGATGTACAGCCGC 1033
Db 969 CCAGAAAGCTCCAGTGTGGGAGGCTCATCATCAACCCCGAGTGTGATGTACAGCCGC 1028
OY 1034 CCAGTGTGGGAAAAAGCTTTTAAACATTCATAGGCAATTGAGCGGATTTGGCGGATTTT 1093
Db 1029 CCAGTGTGGGAAAAAGCTTTTAAACATTCATAGGCAATTGAGCGGATTTGGCGGATTTT 1088
OY 1094 GAGACAATCTTTTATGATTTATGAGCGGATACCAAGTAAAGAAAGTATTTCTCATCC 1153
Db 1089 GAGACAATCTTTTATGATTTATGAGCGGATACCAAGTAAAGAAAGTATTTCTCATCC 1148
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Db 1149 AAATATGACTCCAAAGACCAAGACATGATGGCTGATGAGAGCTGCAAAAGCTTCT 1208
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Db 1209 GACTTTCAACGACTAGTGAACCAAGTGTGTGCGCAACCCAGGCAATGATCTGCAGCC 1268
OY 1274 AGAACAGCTCTGCTGGATTTCCGGGTGGGGGCGCACCGAGGAGAAAGGAGAGACTCAGA 1333
Db 1269 AGAACAGCTCTGCTGGATTTCCGGGTGGGGGCGCACCGAGGAGAAAGGAGAGACTCAGA 1328
OY 1334 AGTGTGAAGCTGCGAAGGTCTTCTATTTAGACACAGAGATGCAACAGATATGT 1393

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Db 1389 CTATGACAACCTGATACACACAGCCATGATGTGCTCCGGCTTCTGACAGGGAGACGTGA 1448
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Db 1569 GAATGTGATGTATTCACGAGACTGATTTATGACAAATGAGGCGACAGCGCTAATCCAC 1628
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OY 1694 TGCATGATTTACTCTTGAAGATGATTCAGAGTCACTCATTTTATTAACAGTGAAT 1753
Db 1689 TGCATGATTTACTCTTGAAGATGATTCAGAGTCACTCATTTTATTAACAGTGAAT 1748
OY 1754 TGTCTGGCTTTTGGCACTCTGTCCATTCGTGACAGGCTGCAAGTGGCTCCCTGCCAGCC 1813
Db 1749 TGTCTGGCTTTTGGCACTCTGTCCATTCGTGACAGGCTGCAAGTGGCTCCCTGCCAGCC 1808
OY 1814 TGTCTCTCCCTTAACCCCTTGTCCGCAAGGGGTATGCGGCTGTGTGTGGCACTGGCGG 1873
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OY 1874 TCAAGTGTGAGAGAGGGGGTGGAGGCTGCCCATTTGAGATCTTCGTGTAGTCTTTC 1933
Db 1869 TCAAGTGTGAGAGAGGGGGTGGAGGCTGCCCATTTGAGATCTTCGTGTAGTCTTTC 1928
OY 1934 CAGGGGCCAATTTTGGATGAGCATGAGCATGTACCTGTACAGCTCTGATGACTTGA 1993
Db 1929 CAGGGGCCAATTTTGGATGAGCATGAGCATGTACCTGTACAGCTCTGATGACTTGA 1988
OY 1994 TGAAGAGAGAGACATGGAAGAGAGACAGCAGCTGACCTGACAGGGCTGCCCTCT 2052
Db 1989 TGAAGAGAGAGACATGGAAGAGAGACAGCAGCTGACCTGACAGGGCTGCCCTCT 2048
OY 2053 GGGGCCACTGTGTATGTGTCGCCAGCTACCTGCTCAACAAGGGGATTTTGTGATGGTTC 2112
Db 2049 GGGGCCACTGTGTATGTGTCGCCAGCTACCTGCTCAACAAGGGGATTTTGTGATGGTTC 2108
OY 2113 TTAGAGCCTTTAGACAGCCCTGATGTGTGCGCAGAAATTAAGGAGCCAGCCCTTCAATGGGTG 2172
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DB 1869 TCAAGTGTGAGAGAGGAGGTGTGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCTTTC 1928
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DB 2109 TTAGAGCTTTACAGCCCTGTGATGTGTGCGCAGAAATTAAGGACCAAGCCCTTATGGGTG 2168
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DB 2228 TATAGACAGTGCCTTGTGGGTGTGAGAGCAATTTGAAGAAAGAACTTCCCTGTAGACATC 2286
OY 2293 CTGTGTGACAGTGTCCACCTGTGACATTTGGGTGGGCTCTGTGGAGGAGACTTACGCTTCC 2352

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Db 2347 TCCCTACATCCCTCCCTGACCCCTGCTCTAGCACCCCTGGAGAGATGACATGCCCTTGGTCT 2406
Oy 2413 GGGCAGGGGGCCCAAGTGTGGACACATGTTGGCTCTTACAGGCTCTAGTCACTGAGAA 2472
Db 2407 GG--CAGGGGGCCCAAGTGTGGACACATGTTGGCTCTTACAGGCTCTAGTCACTGAGAA 2464
Oy 2473 TTGAGTTCATGGGGGAAATCAAGATGCTCACTTAAGTTAAGTACACTGTTTCCATGTTATG 2532
Db 2465 TTGAGTTCATGGGGGAAATCAAGATGCTCACTTAAGTTAAGTACACTGTTTCCATGTTATG 2524
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Db 2585 CCACCTTCACTTAACTCTTGAAGCTGTATCATCTTGGCAAGTAAGAGTGGGCTAT 2644
Oy 2653 TTGAGTCTTGTACAAATGACTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2712
Db 2645 TTGAGTCTTGTACAAATGACTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2704
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Db 2705 AAGCAAGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2764
Oy 2773 GTGGTCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2832
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Db 3185 ATTAATATGCGATTTTTTTTTTCAAGTAA 3214

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RESULT 15

AA290478

AC AA290478;

DT 06-JUN-2000 (first entry)

DE 0vrl15 homolog protein encoding cDNA.

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XX CSg; cancer specific gene; cancer; gynecologic cancer; ovarian; breast;
KM endometrial; uterine; lung; cytotoxic; ss.
XX Homo sapiens.
XX WO200012758-A1.
XX 09-MAR-2000.
XX 01-SEP-1999; 99WO-US19655.
XX 02-SEP-1998; 98US-0098880.
XX (DIAD-) DIADEXUS LLC.
XX Salceda S, Sun Y, Reclipon H, Caferkey R;
XX WPI: 2000-256657/22.
XX P-PSDB: AAY57280.
XX
XX Diagnosing, staging, monitoring, imaging and treating cancer especially
XX gynecological cancers e.g. breast, ovarian cancer and lung cancer,
XX involves measuring cancer specific gene levels in cells and body fluids
XX
XX Claim 9; Page 49-50; 58pp; English.
XX
XX The invention relates to detecting, diagnosing metastasis and staging
XX cancer by measuring levels of cancer specific genes (CSG) in cells,
XX tissues or body fluids. Their remission and progression, decreases and
XX increases in CSG levels, is also monitored, by periodic sample analysis.
XX The methods are useful for detecting cancers, especially gynecologic
XX cancers which include ovarian, breast, endometrial and uterine cancer
XX and lung cancer. Antibodies against the CSgs labeled with paramagnetic
XX ions or a radioisotope is useful for imaging cancer and when conjugated
XX with a cytotoxic agent are useful for treating cancer. The present
XX sequence represents a Ovr115 homolog protein encoding cDNA, that
XX can be used for the detection of the various cancers.
XX
XX Sequence 2479 BP; 578 A; 650 C; 677 G; 574 T; 0 other;
XX
XX Query Match 67.1%; Score 2309.4; DB 21; Length 2479;
XX Best Local Similarity 98.6%; Pred. No. 0;
XX Matches 2425; Conservative 0; Mismatches 21; Indels 13; Gaps 9;
XX
Oy 93 GTCAATATGAACATTCACATACCTATACATGCTGTTGATTAAGCAAGATG 152
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Oy 153 CTTTGAACCTAGAGGTGACACAGCTATGACCTTATGAAAACCATGATACCAAC 212
Db 61 CTTTGAACCTAGAGGTGACACAGCTATGACCTTATGAAAACCATGATACCAAC 120
Oy 213 CGGAAAACCCCTATCCGACAGCCCACTGTGTCCACATGCTGTACAGAGTCAATCCG 272
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Db 181 CTGAGTACTACCCGCTCCCGCCGACAGTACGCGCCGAGAGGTCTCTAGCAGAGCTTCCA 240
Oy 333 ACCCGCTGCTGACAGCAGCCCAATCCCATCCGAGAGTGTGCACTCAAGACTA 392
Db 241 ACCCGCTGCTGACAGCAGCCCAATCCCATCCGAGAGTGTGCACTCAAGACTA 300
Oy 393 AGAAGACACTGTGATACCTTGAACCTGGGAGCTTCTCTGAGGAGCTGCGCTGGCG 452
Db 301 AGAAGACACTGTGATACCTTGAACCTGGGAGCTTCTCTGAGGAGCTGCGCTGGCG 360
Oy 453 CTGCGCTACTCTGGAAGTATGAGGAGCAAGTGTCTCAACTTGGATAGAGTGGACT 512
Db 361 CTGCGCTACTCTGGAAGTATGAGGAGCAAGTGTCTCAACTTGGATAGAGTGGACT 420

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OY	573	GGAGAGAGCAATATCGGTGTGTGGCTCTACGAGCAAACTCATCTTCAGGTACT	632
Db	481	GGAGAGAGCAATATCGGTGTGTGGCTCTACGAGCAAACTCATCTTCAGGTACT	540
OY	633	CATCTCAGAGGAAGTCTGTGGCACTCTGTGTCCAGACGACTGGAAAGAACTACGGGC	692
Db	541	CATCTCAGAGGAAGTCTGTGGCACTCTGTGTCCAGACGACTGGAAAGAACTACGGGC	600
OY	693	GGGGGGCCTTCGAGGAGACATGGGGCTATTAAGAAATATTTTACTCTACCAAGGAATAGTG	752
Db	601	GGGGGGCCTTCGAGGAGACATGGGGCTATTAAGAAATATTTTACTCTACCAAGGAATAGTG	660
OY	753	ATGACAGCGGATCCACGAGCTTTATGAACTGAACACAAAGTGCCGGCAATGTGATATCT	812
Db	661	ATGACAGCGGATCCACGAGCTTTATGAACTGAACACAAAGTGCCGGCAATGTGATATCT	720
OY	813	ATTAATAAATCTACCACAGAGAGCCGTCTCTCAAAAGAGAGTTCCTTTACGCTGTA	872
Db	721	ATTAATAAATCTACCACAGAGAGCCGTCTCTCTCAAAAGAGAGTTCCTTTACGCTGTT	780
OY	873	TAGCCTGGGGGGTCACTTGTAACCTCAAGCCGACAGAGAGAGATCGTGGCGGACAGAGG	932
Db	781	TAGCCTGGGGGGTCACTTGTAACCTCAAGCCGACAGAGAGAGATCGTGGCGGAGAGG	840
OY	933	CGCTCCCGGGGGCCTGGCCCTGGGGAGAGTGAAGCTGACAGTCCAGAGCTCCACGTGTGC	992
Db	841	CGCTCCCGGGGGCCTGGCCCTGGGGAGAGTGAAGCTGACAGTCCAGAGCTCCACGTGTGC	899
OY	993	GGAGGCTCATCATCACCCCGAGATGTGATGTGACAGCCGACCGCTGCGTGAAGAAACT	1053
Db	900	GGAGGCTCATCATCACCCCGAGATGTGATGTGACAGCCGACCGCTGCGTGAAGAAACT	959
OY	1053	CTTAACAATCCATGAGCATTTGGAGGGCATTTTGGGGGATTTTGAGACAAATCTTTCATGTT	1113
Db	960	CTTAACAATCCATGAGCATTTGGAGGGCATTTTGGGGGATTTTGAGACAAATCTTTCATGTT	1013
OY	1113	TATGAGAGCCGATATCAAGATGAAAGAAAGTATTTTCATCCAAATATATGATCCAAAGAC	1173
Db	1020	TATGAGAGCCGATATCAAGATGAAAGAAAGTATTTTCATCCAAATATATGATCCAAAGAC	1073
OY	1173	AAGAACTATGACATTTGGCTGTATGATGAAGCTTCAGAGAGCTCTGACTTTCAACGACCTAGTG	1233
Db	1080	AAGAACTATGACATTTGGCTGTATGATGAAGCTTCAGAGAGCTCTGACTTTCAACGACCTAGTG	1133
OY	1233	AACACAGGTGTCGTGCCCAACCCAGGATATGCTGTACAGCAGAAAGAGCTGTGTGATG	1293
Db	1140	AACACAGGTGTCGTGCCCAACCCAGGATATGCTGTACAGCAGAAAGAGCTGTGTGATG	1193
OY	1293	TCCGGGTGGGGGGCCACCGAGAGAAAGGAGAAACCTCAGAAAGTGTGAAAGCTGCAAG	1353
Db	1200	TCCGGGTGGGGGGCCACCGAGAGAAAGGAGAAACCTCAGAAAGTGTGAAAGCTGCAAG	1253
OY	1353	GTGCTTCTCATTTGAGACACAGAGATGACACAGCAGATATGTCTATGACAACTGATCACA	1413
Db	1260	GTGCTTCTCATTTGAGACACAGAGATGACACAGCAGATATGTCTATGACAACTGATCACA	1313
OY	1413	CCAGCATGATCTGTGCGGGCTTCTGTGCAAGGGAAAGTGTGATTTCTTGCCAGGGGTGACAT	1473
Db	1320	CCAGCATGATCTGTGCGGGCTTCTGTGCAAGGGAAAGTGTGATTTCTTGCCAGGGGTGACAT	1373
OY	1473	GGAGGGCCTTGTGCTCACTTGGAAAGCAATATGTGTGGCTGTATAGGGATACAAAGCTGG	1533
Db	1380	GGAGGGCCTTGTGCTCACTTGGAAAGCAATATGTGTGGCTGTATAGGGATACAAAGCTGG	1433
OY	1533	GGTTCCTGGCTGTGCCAAAGCTTACAGACCAAGAGTGTACGGGAATGTGATTTATTCACG	1593
Db	1440	GGTTCCTGGCTGTGCCAAAGCTTACAGACCAAGAGTGTACGGGAATGTGATTTATTCACG	1493

QY	1593	GATGGATTTATGCAAAATGAGGGCAGACGGCTAATCCACATGGGTCTCGCTTGACG	1653
Db	1500	GACGTGATTTATCGACAAATGAAGGCAAAAGGGCTAATCCACATGGGTCTCGCTTGGACG	1559
QY	1653	TGCTTTTATCAAGAAACAAATGAGGGGTGGTTTTCCTTCCCGCGACATGATTTACTTTAGA	1712
Db	1560	TCGTTTATCAAGAAACAAATGAGGGGTGGTTTTCCTTCCCGCGACATGATTTACTTTAGA	1619
QY	1713	GATGATTCAGAGGTCACTTCATTTTATTAACAGTGAACCTTGTGCTGGCTTGGCACCTC	1772
Db	1620	GATGATTCAGAGGTCACTTCATTTTATTAACAGTGAACCTTGTGCTGGCTTGGCACCTC	1679
QY	1773	CTGGCATTCGTGAGGCTCGACGTGGCTGCCCGCCACCGCTCTCCCTAACCCCTTG	1832
Db	1680	CTGGCATTCGTGAGGCTCGACGTGGCTGCCCGCCACCGCTCTCCCTAACCCCTTG	1739
QY	1833	TCCCAAGGGGTGATGTGGCGCTGGTTGTGAGGACATGGCGGCTCAAGTGTGA--GGAAG	1890
Db	1740	TCCCAAGGGGTGATGTGGCGCTGGTTGTGAGGACATGGCGGCTCAAGTGTGAAG	1799
QY	1891	GGGTGAGGCTG--CCCATTTGAGATCTTCCCTGCTGAGTCCCTTCCAGGGGCCAATTTTGG	1949
Db	1800	GGTTGAGGCTGCCCCCATTTGAGATCTTCCCTGCTGAGTCCCTTCCAGGGGCCAATTTTGG	1859
QY	1950	ATGAGCATGAGAGCTGTACCTCTCAGCTGCTGGATACCTTGAGATGAAAAAGAGACACA	2009
Db	1860	ATGAGCATGAGAGCTGTACCTCTCAGCTGCTGGATACCTTGAGATGAAAAAGAGACACA	1919
QY	2010	TGGAAGAGGAGACAGCCAGGTGGACCTGACCTGAGGGGCTG--CTCTGGGGCCACTTGGTAGT	2068
Db	1920	TGGAAGAGGAGACAGCCAGGTGGACCTGAGGGGCTGCTCTGGGGCCACTTGGTAGT	1979
QY	2069	GTCCCCAGCCTACCTCTCCACAAGGGGATTTTGTGATGGGTTCTTAAAGCCCTTAGACGC	2128
Db	1980	GTCCCCAGCCTA---CTTCAACAAGGGGATTTTGTGATGGGTTCTTAAAGCCCTTAGACGC	2036
QY	2129	CCCTGATGTGGCCCAAGAAATTAAGAGGACACGCCCTTCATGGGTGGTGAAGTGGTATAC	2188
Db	2037	CCCTGATGTGGCCCAAGAAATTAAGAGGACACGCCCTTCATGGGTGGTGAAGTGGTATAC	2095
QY	2189	CTTTTAAGGGGACAGACAATCTTTTGTCTTATGCGGTGAGAAATATAGACAGTACCTCT	2248
Db	2096	CTTTTAAGGGGACAGACAATCTTTTGTCTTATGCGGTGAGAAATATATAGACAGTACCTCT	2155
QY	2249	GGGTGCGAGGAGCAATTGAAAAAGGAACCTTGGCCCTGAGCAGCTCTCGTGAGGTCTCCA	2308
Db	2156	-GGTGCAGAGGAGCAATTGAAAAAGGAACCTTGGCCCTGAGCAGCTCTCGTGAGGTCTCCA	2214
QY	2309	CCCTGACATTTGGGGGGGGGCTCTGGGAGGGAGACTAGGCTTCTCTCTCATCTCCCTCGA	2368
Db	2215	CCCTGACATTTGGGGGGGGGCTCTGGGAGGGAGACTAGGCTTCTCTCTCATCTCCCTCGA	2274
QY	2369	CCCTGCTCTAGCACCTCTGAGAGTGCACATGCGCCCTTGGTCTCTGGGCGAGGGGCCCAAG	2428
Db	2275	CCCTGCTCTAGCACCTCTGAGAGTGT--AATGCGCTTGGTCTCTGGCA--GGGCGCCAAAG	2331
QY	2429	TTCTGGCACCATGTTGGCCTCTTTCAGGCGCTGCTAAGTCACTGGAATTAAGTCCATGCGGG	2488
Db	2332	TTTGGCACCATGTTGGCCTCTTTCAGGCGCTGATAGTCACTGGAATTAAGTCCATGCGGG	2391
QY	2489	AAATCAAGAGTGCACAGTTTAAAGTACACGTCTTCCATGTATATGTTTCTACACATTCGT	2547
Db	2392	AAATCAAGAGTGCACAGTTTAAAGTACACGTCTTCCATGTATATGTTTCTACACATTCGT	2450

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Search completed: January 15, 2003, 18:35:18
Job time : 646 secs
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OY	453	CTGGCTCTCTCTGGAAAGTTCATGCGGACGACGAAGTCCCACTCTCGGGATATGACTGGACG	512
Dp	351	CTGGCTCTCTCTGGAAAGTTCATGCGGACGACGAAGTCTCAACTCTGGATATGATGGACCT	420
OY	513	CCTGAGTACCTGCATCAACCCCTCTAAGTGGTGTATGGCGTGCACATGCCCCGGCG	572
Dp	421	CCCTGAGTACCTGCATCAACCCCTCTAAGTGGTGTATGGCGTGCACATGCCCCGGCG	480
OY	573	GGGAGGAGGAAATCGGGTGTGGCTCTACAGGACCAACTCATCTCAGTGTACT	632
Dp	481	GGGAGGAGGAAATCGGGTGTGGCTCTACAGGACCAACTCATCTCAGTGTACT	540
OY	633	CATCTCAGAGGAAGTCTCTGGCACCCTCTGTGCCAAGACGACTGGAAAGTACGGCG	692
Dp	541	CATCTCAGAGGAAGTCTCTGGCACCCTCTGTGCCAAGACGACTGGAAAGTACGGCG	600
OY	693	GGGGGGCCCTGCAGGAGCAATGGGGCTATTAAGATAATTTTTTACTAGCCAAAGAAATGTGG	752
Dp	601	GGGGGGCCCTGCAGGAGCAATGGGGCTATTAAGATAATTTTTTACTAGCCAAAGAAATGTGG	660
OY	753	ATGACAGCGGATATCCACCAAGCTTTATGAACTGAAACCAAGTGGCGGAATGTGAATATCG	812
Dp	661	ATGACAGCGGATATCCACCAAGCTTTATGAACTGAAACCAAGTGGCGGAATGTGAATATCT	720
OY	813	ATAAAAAACTGTACACAGTGTATGCTTTCTTCAAAAAGCAGTGGTTTTCTTACGCTGTA	872
Dp	721	ATAAAAAACTGTACACAGTGTATGCTTTCTTCAAAAAGCAGTGGTTTTCTTACGCTGTT	780
OY	873	TAGCCTGGGGGGTCACTGTGAACCAACCGCCGACAGACAGATCTGGGGGGGACAGCG	932
Dp	781	TAGCCTGGGGGGTCACTGTGAACCAACCGCCGACAGACAGATCTGGGGGGGACAGCG	840
OY	933	CGCTCCCGGGGGCCCTGGGCCCTGGGACAGTCAAGCTTGACAGCTCCAGAACTGCACGTGTGC	992
Dp	841	CGCTCCCGGGGGCCCTGGGCCCTGGGACAGTCAAGCTTGACAGCTCCAGAACTGCACGTGTGC	899
OY	993	GGAGGCTTCATATACACCCCCGAGTGGATGTGTACACAGCCCCCACTGCGTGGAAAAACT	105
Dp	900	GGAGGCTTCATATACACCCCCGAGTGGATGTGTACACAGCCCCCACTGCGTGGAAAAACT	959
OY	1053	CTTAAACATCCATGGCATTTGGACCGCATTTTGGCGGATTTTGGAGACAAATTTTCATGTTT	111
Dp	960	CTTAAACATCCATGGCATTTGGACCGCATTTTGGCGGATTTTGGAGACAAATTTTCATGTTT	101
OY	1113	TATGAGAGCCGGATATCCAAAGTAAAGTATTTCTCATCCAAATTTATGACTCCAAAGCC	117
Dp	1020	TATGAGAGCCGGATATCCAAAGTAAAGTATTTCTCATCCAAATTTATGACTCCAAAGCC	107
OY	1173	AAGAAACATATGATTTGGCGGTATGAACCTGCAGAAAGCTCTGACTTTCAACGACCTAATG	123
Dp	1080	AAGAAACATATGATTTGGCGGTATGAACCTGCAGAAAGCTCTGACTTTCAACGACCTAATG	113
OY	1233	AAACCAAGTGTCTGTGCCCAACCCAGGCGATATGCTGCAGCCAGAAAGCTGTGCTGATTT	129
Dp	1140	AAACCAAGTGTCTGTGCCCAACCCAGGCGATATGCTGCAGCCAGAAAGCTGTGCTGATTT	119
OY	1293	TCCGGGTGGGGGGCCACCGAGAGGAAAGGAAAGACCTCABAATGCTGMAACGTGCCAAG	135
Dp	1200	TCCGGGTGGGGGGCCACCGAGAGGAAAGGAAAGACCTCABAATGCTGMAACGTGCCAAG	125
OY	1353	GTGCTTCTCATTTGAGACACAGATATGCAACAGCATATGTCTATGCAACCTGATCACA	141
Dp	1260	GTGCTTCTCATTTGAGACACAGATATGCAACAGCATATGTCTATGCAACCTGATCACA	131
OY	1413	CCAGCCATGATCTGTGCCCGCTTCTGTCTCAGGGGAACGTGATTTCTTGGCAGGGTGACAGT	147
Dp	1320	CCAGCCATGATCTGTGCCCGCTTCTGTCTCAGGGGAACGTGATTTCTTGGCAGGGTGACAGT	137
OY	1473	GGAGGGGCTCTGGTCACTGTGAAACAAATATCTGGTGGCTGTATAGGGATATCAACTGG	153
Dp	1380	GGAGGGGCTCTGGTCACTGTGAAACAAATATCTGGTGGCTGTATAGGGATATCAACTGG	143

OY	1533	GGTCTCTGGCTGGCCAAAGCTTTACAGCCAGAGAGTGTACGGGAATGATGATTTACAG	1592
OY	1533	GGTCTCTGGCTGGCCAAAGCTTTACAGCCAGAGAGTGTACGGGAATGATGATTTACAG	1592
Db	1440	GGTCTCTGGCTGTGCCAAAGCTTACAGACCAGAGGTGTACGGGAATGTATGTTATTCAG	1499
OY	1593	GACTGGATTTATTCACAAATGAGGGCAGAGAGGCTAATCCATAGTCTTCTGCTTGAAG	1652
Db	1500	GACTGGATTTATTCACAAATGAGGGCAGAGAGGCTAATCCATAGTCTTCTGCTTGAAG	1555
OY	1653	TGCTTTTTCACAAGAAACATATGGGGCTGTGTTTGTCTTCCCGGTGATGATTTACTTTAGA	1711
Db	1560	TGCTTTTTCACAAGAAACATATGGGGCTGTGTTTGTCTTCCCGGTGATGATTTACTTTAGA	1619
OY	1713	GATGATTTACAGAGGTCACTTTCATTTTATTTAAACAGTAACCTGTGTGGCTTTGGACACT	1772
Db	1620	GATGATTTACAGAGGTCACTTTCATTTTATTTAAACAGTAACCTGTGTGGCTTTGGACACT	1675
OY	1773	CTGCATTTCTGTGCAAGGCTCAGTGTGCTCCCTCCCGCCAGCCTGTCTCCCTTAACCCCTTGG	1833
Db	1680	CTGCATTTCTGTGCAAGGCTCAGTGTGCTCCCTCCCGCCAGCCTGTCTCCCTTAACCCCTTGG	1733
OY	1833	TCCGCAAGGGGTGTATGGCCGCTGTGTTGTGGGCATGTGGCGGTCAAGTGTGA - GGAAG	1890
Db	1740	TCCGCAAGGGGTGTATGGCCGCTGTGTTGTGGGCATGTGGCGGTCAATTTGGAAAGGAAG	1799
OY	1891	GGGTGGAGGCTG - CCCATTTGAATCTTCTGTGAGTCTCTTCCAGGGGCCAATTTTGG	1948
Db	1800	GGTTTGGAGGCTGCCCCCATTTGAATCTTCTGTGTGAGTCTCTTCCAGGGGCCAATTTTGG	1855
OY	1950	ATGAGCATGAGAGCTGTACCTCTCAGCTGTGTGATACATTGAATATAAAAGAGAGACA	2005
Db	1860	ATGAGCATGAGAGCTGTACCTCTCAGCTGTGTGATACATTGAATATAAAAGAGAGACA	1915
OY	2010	TGGAAGAGGAGACAGCCAGGTGTGCACCTGTGACGCGCTG - CCTGTGGGCCACTTGGTAGT	2066
Db	1920	TGGAAGAGGAGACAGCCAGGTGTGCACCTGTGACGCGCTGTGAGGCTGTGGGCTTGGTAGT	1979
OY	2069	GTCCCCAGCCTACTCTCTCCACAAGGGGATTTTCTATGSGGTTCTTAAAGCCTTAGCAC	2122
Db	1980	GTCCCCAGCCTTA - -CTTCAACAAGGGGATTTTCTATGSGGTTCTTAAAGCCTTAGCAC	2036
OY	2129	CCTGGATGTGGGCCAGAAATTAAGAGGACAGCCCTTCATGTGGGGGAGAGCTGTGTAGTGC	2188
Db	2037	CCTGGATGTGTGGGCCAGAAATTAAGAGGACAGCCCTTCATGTGGGGGAGAGCTGTGTAGTGC	2099
OY	2189	CTTGTAAAGGGGAAACAGAAACATTTTGTCTTATGGGGGTAGAAATATAGACAGTCCCTT	2248
Db	2096	CTTGTAAAGGGGAAACAGAAACATTTTGTCTTATGGGGGTAGAAATATAGACAGTCCCTT	2155
OY	2249	GGGTGGCAGGGGAAGCAATTTAAAGAGACATCTCCCTGTAGACACTCTGTGTGCAGGTGTCA	2306
Db	2156	-GGGTGGCAGGGGAAGCAATTTAAAGAGACATCTCCCTGTAGACACTCTGTGTGCAGGTGTCA	2214
OY	2309	CTGTACATTTGGGGGGGGGCTGTGGGAGGGAAGCTAGAGCTTCCTCTCATCTCCCTGA	2366
Db	2215	CTGTACATTTGGGGGGGGGCTGTGGGAGGGAAGCTAGAGCTTCCTCTCATCTCCCTGA	2274
OY	2369	CCCTGTCTCTAGCACCTGTGAGAGATGTACATCTGCCCTTGTGTCTGTGGGAGGGGCCCAAG	2428
Db	2275	CCCTGTCTCTAGCACCTGTGAGAGATG - AATGCCCTTGTGTCTGTGGCA - GGGGCCCAAG	2333
OY	2429	TCTGGCACCATGTGGCTCTTTCAGGCGCTGTAGTCACTGTGAATTTGAGTCCATGGGG	2488
Db	2332	TTTGGCACCATGTGGCTCTTTCAGGCGCTGTAGTCAATTTGGAATTTGAGTCCATGGGG	2391
OY	2489	AAATCAAGAGATGCTCAATTTAAGGTACATCTGTTCATGTATGTTTCTACACATTTGCT	2547
Db	2392	AAATCAAGAGATGCTCAATTTAAGGTACATCTGTTCATGTATGTTTCTACACATTTGAT	2450

RESULT 2
US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 6444419

QY	813	ATAAAAACGTGTACCAAGATGAGCGCTGTTCTTCAAAACAGTGGTTTCTTTACCGTGA	872
Db	721	ATAAAAACGTGTACCAAGATGAGCGCTGTTCTTCAAAACAGTGGTTTCTTTACCGTGT	780
QY	873	TAGCGCTGCGGGGTCAACTTGAATCACTCAAGCCGCGACAGAGATCGTGGCGCGAGAGCG	932
Db	781	TAGCGCTGCGGGGTCAACTTGAATCAAGCCGCGACAGAGATCGTGGCGGTGAGAGCG	840
QY	933	CGCTCCGGGGGCGCTGGCGCTGGGCGAGGTTCAGCTGCACGTCCAGAACGTCCACGTGTGC	992
Db	841	CGCTCCGGGGGCGCTGGCGCTT - GGACAGTTCAGCTGCACGTCCAGAACGTCCACGTGTGC	899
QY	993	GGAGGCTTCATCATCACACCCCCAGAGTGGATGTGTACAGCCGCCCATCTGCTGGAAAAACT	1053
Db	900	GGAGGCTTCATCATCACACCCCCAGAGTGGATGTGTACAGCCGCCCATCTGAAAAAAGCT	959
QY	1053	CTTAAACATCCATGAGCATTTGGACGGCATTTTGGCGGAGATTTTGGAGCAATCTTTCATGTGTC	1112
Db	960	CTTAAACATCCATGAGCATTTGGACGGCATTTTGGCGGAGATTTTGGAGCAATCTTTCATGTTC	1019
QY	1113	TATGAGAGCGGATATCAAGATGAAAAAGTATTTTCATATCCAAATYTATGACTCCAAAGAC	1172
Db	1020	TATGAGAGCGGATATCAAGATGAAAAAGTATTTTCATATCCAAATYTATGACTCCAAAGAC	1079
QY	1173	AAGAAACATGACATTTGGCGGTGATGAACTGACAAACCTCTGACTTTCAAGACTAGTG	1232
Db	1080	AAGAAACATGACATTTGGCGGTGATGAACTGACAAACCTCTGACTTTCAACACCTAGTG	1139
QY	1233	AAACAGATGTCGTGCGCCCAACCCAGGATGATCTGCACCGAAGACGTCTGCTGGAGATT	1292
Db	1140	AAACAGATGTCGTGCGCCCAACCCAGGATATATCTGCAGCAGAAAGCTCTGCTGGAGATT	1199
QY	1293	TCCGGGTGGGGGGCCACCGAGAGAAAGGAGAACCTCAGAAAGTGTGTGACCTCCCAAG	1352
Db	1200	TCCGGGTGGGGGGCCACCGAGAGAAAGGAGAACCTCAGAAAGTGTGTGACCTCCCAAG	1259
QY	1333	GTGCTTCTCATTTGAGACACAGAGATGCACAGCAGATATGTCTATGACAACTGATCA	1412
Db	1260	GTGCTTCTCATTTGAGACACAGAGATGCACAGCAGATATGTCTATGACAACTGATCA	1319
QY	1413	CCAGCAGATGATCTGTGCGGCTTCGTGACGGGAACTGGATTTCTTGGCCAGGGGTACAGT	1472
Db	1320	CCAGCAGATGATCTGTGCGGCTTCGTGACGGGAACTGGATTTCTTGGCCAGGGGTACAGT	1379
QY	1473	GGAGGGGCTCTGTGCTTTCGAAGAACCAATATCTGTGCTGTATAGGGATATCAAGCTGG	1532
Db	1380	GGAGGGGCTCTGTGCTTTCGAAGAACCAATATCTGTGCTGTATAGGGATATCAAGCTGG	1439
QY	1533	GGTTCGTGGCTGTGCCAAGCTTACAGACCGAGAGTGTACGGGAATGTGATTTACAG	1592
Db	1440	GGTTCGTGGCTGTGCCAAGCTTACAGACCGAGAGTGTACGGGAATGTGATTTACAG	1499
QY	1593	GACGTGAGTTATGCAAAATGAGGGGACAGCGGTATATCCAAATGGTCTTGGCTTTGACG	1653
Db	1500	GACGTGAGTTATGCAAAATGAGGGGACAAAGGCTAATATCCAAATGGTCTTGGCTTTGACG	1559
QY	1653	TGCTTTTACAGAAACAATGGGGGCTGTTTGGCTTCCCGTGACATATTTACTTTAGA	1712
Db	1560	TGCTTTTACAGAAACAATGGGGGCTGTTTGGCTTCCCGTGACATATTTACTTTAGA	1619
QY	1713	GATGATTCAGAGGTCACTTCATTTTATTAACAGTGAACTGTGTCGGTCTTGGACACT	1772
Db	1620	GATGATTCAGAGGTCACTTCATTTTATTAACAGTGAACTGTGTCGGTCTTGGACACT	1679
QY	1773	CTGCGCATTCGTGTGAGGCTGTGAGTGGCTTCCCGTCCGCAACGTCTCTCCCTAACCCCTTG	1832
Db	1660	CTGCGCATTCGTGTGAGGCTGTGAGTGGCTTCCCGTCCGCAACGTCTCTCCCTAACCCCTTG	1739
QY	1833	TCCCGAAGGGGTGAATGCGCGCGGTGTGTGTGGGACATGGCGTCAAGTGTGA - GGAGAG	1890
Db	1740	TCCCGAAGGGGTGAATGCGCGCGGTGTGTGTGGGACATGGCGTCAATTTGTGAAGGAAGAG	1799
QY	1891	GGGTGGAGGCTG - CCCCATTGAGATCTCTCCGTGAGTCCCTTTCCAGGGGGCAATTTTGG	1949

Db	1800	GCCTTGGAGGGCCGCCCATTTGAGATCTCTCTGTGAGTCTTTCCAGGGGCCAATTTTGG	1855
Qy	1950	ATGAGCATGAGAGCTGTACCTCTTCAGCTGCTGGATGACTTGAATGAAAAAGAGACACA	2009
Db	1860	ATGAGCATGAGAGCTGTACCTCTTCAGCTGCTGGATGACTTGAATGAAAAAGAGAGACA	1919
Qy	2010	TGAGAAAGGAGACAGCCAGGTGGCAGCTGAGAGGGGTG--CCCTGGGGCAGCTTGGTAGT	2068
Db	1920	TGAGAAAGGAGACAGCCAGGTGGCAGCTGAGAGGGGTG--CCCTGGGGCAGCTTGGTAGT	1979
Qy	2069	GTCCCAACGCTTACCTCTCCACAAGGGGATTTTCTGATGGGTCTTACAGCCCTTAGCAGC	2128
Db	1980	GTCCCAACGCTTACCTCTCCACAAGGGGATTTTCTGATGGGTCTTACAGCCCTTAGCAGC	2038
Qy	2129	CCTGGATGGTGGGCCAGAAATTAAGAGGACAGCCCTCATGGGTGGAGCGTGGTGTAC	2188
Db	2037	CCTGGATGGTGGGCCAGAAATTAAGAGGACAGCCCTCATGGGTGGAGCGTGGTGTAC	2095
Qy	2189	CTTGTAAAGGGAAACAGAAACATTTTGTCTTAATGGGATGAGAAATATAGACAGTCCCTT	2248
Db	2096	CTTGTAAAGGGAAACAGAAACATTTTGTCTTAATGGGATGAGAAATATAGACAGTCCCTT	2155
Qy	2249	GGGGCCAGAGGAAAGCAATTAAAAAGAACTGGCCCTGACACTCCTGGTGGAGAGTCTCCA	2308
Db	2156	-GGTGCAGAGGAAAGCAATTAAAAAGAACTGGCCCTGACACTCCTGGTGGAGAGTCTCCA	2214
Qy	2309	CCTGCACATTGGGTGGGGGCTCTGGGAGGAGAGCTAGGCTTCTCTCTATCTCTCCCTGA	2368
Db	2215	CCTGCACATTGGGTGGGGGCTCTGGGAGGAGAGCTAGGCTTCTCTCTATCTCTCCCTGA	2274
Qy	2369	CCCTGCTCTCAGACACCTTGGAGATGCACATGCCCCCTTGGTCTCTGGCGAGGGGCCCAAG	2428
Db	2275	CCCTGCTCTCAGACACCTTGGAGATG--ATGCGCCCTTGGTCTCTGGCGA--GGGCGCCAAAG	2331
Qy	2429	TCTGGCAGCAGTTTGGGCTCTTCAGGCGTGGTAGTCACTGGAATAATGAGGTCATGGGGG	2488
Db	2332	TTTGGCAGCAGTTTGGGCTCTTCAGGCGTGGTATGTCATTGGAATAATGAGGTCATGGGGG	2391
Qy	2489	AAATCAAGAGTGCCTCAAGTTTAAAGTACACTGTTTCCATGTATGTTTCAACACATTGCT	2547
Db	2392	AAATCAAGAGTGCCTCAAGTTTAAAGTACACTGTTTCCATGTATGTTTCAACACATTGAT	2450

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RESULT 3
: Sequence 1, Application US/09342749
: Patent No. 6166194
: GENERAL INFORMATION:
: APPLICANT: Wong, Alexander K.C.
: APPLICANT: Tavtigian, Sean V.
: APPLICANT: Teng, David H.-F.
: APPLICANT: Myriad Genetics, Inc.
: TITLE OF INVENTION: TPMSRS2 is a Tumor Suppressor
: FILE REFERENCE: 2318-202
: CURRENT APPLICATION NUMBER: US/09/342,749
: CURRENT FILING DATE: 1999-06-29
: EARLIER APPLICATION NUMBER: US 60/091,044
: EARLIER FILING DATE: 1998-06-29
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1479
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1476)
: FEATURE:
: NAME/KEY: conflict
: LOCATION: (724)
: OTHER INFORMATION: Listed as T in GenBank Accession NO. 075329
: FEATURE:

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1 NAME/KEY: conflict
2 LOCATION: (985)
3 OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
4 FEATURE:
5 NAME/KEY: conflict
6 LOCATION: (1347)
7 OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
8 FEATURE:
9 NAME/KEY: conflict
10 LOCATION: (1466)
11 OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329
12 FEATURE:
13 NAME/KEY: conflict
14 LOCATION: (1471)
15 OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329.
16 FEATURE:
17 NAME/KEY: allele
18 LOCATION: (478)
19 OTHER INFORMATION: This base can be G or A with G being the more
20 OTHER INFORMATION: common allele. The codon will change from Val to
21 OTHER INFORMATION: Met.
22 FEATURE:
23 NAME/KEY: allele
24 LOCATION: (777)
25 OTHER INFORMATION: This base can be C or T with C being the more
26 OTHER INFORMATION: common allele. The codon is unaffected with both
27 OTHER INFORMATION: alleles encoding Gly.
28 FEATURE:
29 NAME/KEY: allele
30 LOCATION: (768)
31 OTHER INFORMATION: This base can be C or T with C being the more
32 OTHER INFORMATION: common allele. This is a silent polymorphism.
33 FEATURE:
34 NAME/KEY: allele
35 LOCATION: (834)
36 OTHER INFORMATION: This base can be C or T with C being the more
37 OTHER INFORMATION: common allele. This is a silent polymorphism.
38 FEATURE:
39 NAME/KEY: allele
40 LOCATION: (625)
41 OTHER INFORMATION: This base can be T or A with T being the more
42 OTHER INFORMATION: common allele. The codon will change from Phe to
43 OTHER INFORMATION: Ile
44
45 US-09-342-749-1

```

	Query Match	Similarity	42.68;	Score 1468;	DB 4;	Length 1479;	
	Best Local	Similarity	99.98;	Pred. No. 0;	Mismatches	0;	Indels 1; Gaps
	Matches 1479;	Conservative					
Qy	149	ATGGCTTTGACCTAGAGGTACACCAACAGCTTTTGGACCTTACATGTAAGAAACATGATGATAC	208				
Db	1	ATGGCTTTGAACCTAGAGGTACACCAACAGCTTTTGGACCTTACATGTAAGAAACATGATGATAC	60				
Qy	209	CAACCGGAAAAACCCCTATCCGGCAGACGCCACTGTGGTCCCACTGTCACAGAGGTGCAT	268				
Db	61	CAACCGGAAAAACCCCTATCCGGCAGACGCCACTGTGGTCCCACTGTCACAGAGGTGCAT	120				
Qy	269	CCGGCTAGTACTACCGGTCCCGCCGTCGCCAGTAGACGCCCGAGAGGTCTGACGACAGCT	328				
Db	121	CCGGCTAGTACTACCGGTCCCGCCGTCGCCAGTAGACGCCCGAGAGGTCTGACGACAGCT	180				
Qy	329	TCCAAACCCCGTCTGTCGACACGACCCCAAAATCCCATCCGAGACAGTGTCCACCTCAAG	388				
Db	181	TCCAAACCCCGTCTGTCGACGACCCCAAAATCCCATCCGAGACAGTGTCCACCTCAAG	240				
Qy	389	ACTAAGAAAGACATGTGCATCACCTGACCCCTGGGACCTTCCCTGTTGGAGAGCTGCCTG	448				
Db	241	ACTAAGAAAGACATGTGCATCACCTGACCCCTGGGACCTTCCCTGTTGGAGAGCTGCCTG	300				
Qy	449	GCCGCTGGCCCTACCTCGGAATCTATGGGACGAAAGTCTCCAAACTCTGGGATGAGATGC	508				
Db	301	GCCGCTGGCCCTACCTCGGAATCTATGGGACGAAAGTCTCCAAACTCTGGGATGAGATGC	360				

509 GACTCCTCAGGTACATCATCAACCCCTCTAAGTGTGATGGCGTGTACACTGCCCC 568
|||||
361 GACTCCTCAGGTACATCATCAACCCCTCTAAGTGTGATGGCGTGTACACTGCCCC 420
569 GCGGGGAGAGCAGAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 628
|||||
421 GCGGGGAGAGCAGAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 480
629 TACTCATCTCAGAGAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 688
|||||
481 TACTCATCTCAGAGAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 540
689 GCGGGGAGAGCAGAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 748
541 GCGGGGAGAGCAGAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 600
749 GTCGATGACAGCGAGATCAGACCTTATGAATGAACAGAGTGGCGGCAATGTGAT 808
|||||
601 GTCGATGACAGCGAGATCAGACCTTATGAATGAACAGAGTGGCGGCAATGTGAT 660
809 ATCTATAAAAAACTGTACACAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 868
661 ATCTATAAAAAACTGTACACAGATGCTGTTCGCTTACGAGCAACCTTCATCTTCAGGTG 720
869 TGTATAGCTGCGGGGTCGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 928
721 TGTATAGCTGCGGGGTCGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 780
929 AGCGGCTGCGGGGTCGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 988
781 AGCGGCTGCGGGGTCGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 839
989 GTCGAGAGCTCCATCATCATCAACCCCTCTAAGTGTGATGGCGTGTACACTGCCCC 1048
840 GTCGAGAGCTCCATCATCATCAACCCCTCTAAGTGTGATGGCGTGTACACTGCCCC 899
1049 ACCTCTTAAACATCATCATCATCAACCCCTCTAAGTGTGATGGCGTGTACACTGCCCC 1108
900 ACCTCTTAAACATCATCATCATCAACCCCTCTAAGTGTGATGGCGTGTACACTGCCCC 959
1109 GTTCTATGAGCGGAGTACCAAGTATGAAAGATTTTCATCAATGATGCTGCA 1168
960 GTTCTATGAGCGGAGTACCAAGTATGAAAGATTTTCATCAATGATGCTGCA 1019
1169 GACCAAGAACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228
1020 GACCAAGAACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
1229 AGTGAAGAACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1288
1080 AGTGAAGAACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
1289 GATTTCCGGGTGGGGGCGCCAGAGAGAAAGGAGAACCTCTGAGAGTGTGTAACGCTGC 1348
1140 GATTTCCGGGTGGGGGCGCCAGAGAGAAAGGAGAACCTCTGAGAGTGTGTAACGCTGC 1199
1349 CAAGGTCTTCTCATGAGACAGAGATGCAACAGCATATGCTATGACAACTGAT 1408
1200 CAAGGTCTTCTCATGAGACAGAGATGCAACAGCATATGCTATGACAACTGAT 1259
1409 CACACAGAGCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1468
1260 CACACAGAGCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319
1469 CAGTGAAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1528
1320 CAGTGAAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1379
1529 CTGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1588
1380 CTGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439
1589 CACGAGCTGATTTATTCAGCAAAATGAGGCGCAGCGCTAA 1628

DB 1440 CACGAGCTGATTTATTCAGCAAAATGAGGCGCAGCGCTAA 1479

RESULT 4
US-09-691-840-1
Sequence 1, Application US/09691840
Patent No. 6444419
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavligian, Sean V.
APPLICANT: Teng, David H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TPRS2 is a Tumor Suppressor
FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/691,840
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US/09/342,749
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/091,044
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1479
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1476)
NAME/KEY: conflict
LOCATION: (724)
OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
NAME/KEY: conflict
LOCATION: (985)
OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
NAME/KEY: conflict
LOCATION: (1347)
OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
NAME/KEY: conflict
LOCATION: (1466)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
NAME/KEY: conflict
LOCATION: (1471)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
NAME/KEY: allele
LOCATION: (478)
OTHER INFORMATION: This base can be G or A with G being the more
OTHER INFORMATION: common allele. The codon will change from Val to
NAME/KEY: allele
LOCATION: (777)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. The codon is unaffected with both
NAME/KEY: allele
LOCATION: (768)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. This is a silent polymorphism.
NAME/KEY: allele
LOCATION: (834)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. This is a silent polymorphism.
NAME/KEY: allele
LOCATION: (625)
OTHER INFORMATION: This base can be T or A with T being the more
OTHER INFORMATION: common allele. The codon will change from Phe to Ile
US-09-691-840-1

Query Match 42.6%; Score 1468; DB 4; Length 1479;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1479; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

149 ATGGCTTGAACACAGGTCACACAGCATTGACCTTACTATGAAACCATGATAC 208
1 ATGGCTTTGAACTAGAGGGTCACACAGCATTGACCTTACTATGAAACCATGATAC 60
209 CAACCGGAAACCCCTATCCGACAGCCACCTGATGTCCTCCACTGTCAGAGGTCAT 268
61 CAACCGGAAACCCCTATCCGACAGCCACCTGATGTCCTCCACTGTCAGAGGTCAT 120
269 CCGGCTCAGTACTACCCGTCGCCCGTCAGTACGCCCGAGGGTCTGACGAGGCT 328
121 CCGGCTCAGTACTACCCGTCGCCCGTCAGTACGCCCGAGGGTCTGACGAGGCT 180
329 TCCAAACCCGTCGTCGACGACGCCAAATCCCATCCGAGACAGTGTGCACTCAAG 388
181 TCCAAACCCGTCGTCGACGACGCCAAATCCCATCCGAGACAGTGTGCACTCAAG 240
389 ACTAAGAAAGCACTGTGATCACTTGAACCTTGGGACCTTCTGAGGAGCTGGCTG 448
241 ACTAAGAAAGCACTGTGATCACTTGAACCTTGGGACCTTCTGAGGAGCTGGCTG 300
449 GCCGCTGGCCTACTGTGAAGTTCAATGGGACAGCAAGTGTCCAACTCTGGATAGATGC 508
301 GCCGCTGGCCTACTGTGAAGTTCAATGGGACAGCAAGTGTCCAACTCTGGATAGATGC 360
509 GACTCTCAGGTCAGTGTGATCAACCCCTTAACCTGTGTGATGGCTGTCACTGCCCC 568
361 GACTCTCAGGTCAGTGTGATCAACCCCTTAACCTGTGTGATGGCTGTCACTGCCCC 420
569 GCGGGGAGAGAGAGAAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 628
421 GCGGGGAGAGAGAGAAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 480
629 TACTCATCTCAGAGAGAAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 688
481 TACTCATCTCAGAGAGAAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 540
689 GCGGGGAGAGAGAGAAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 748
541 GCGGGGAGAGAGAGAAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 600
749 GTGATGACAGGAGATCCACGAGCTTATGAAATGAAACAAAGTGGCGGCAATGCGAT 808
601 GTGATGACAGGAGATCCACGAGCTTATGAAATGAAACAAAGTGGCGGCAATGCGAT 660
809 ATCTATATAAACTGTACACAGTATGCTGTCTTCAAAAGCAGTGTCTTTTACGC 868
661 ATCTATATAAACTGTACACAGTATGCTGTCTTCAAAAGCAGTGTCTTTTACGC 720
869 TGTATAGCTGCGGGGTCACTTGAATCTGACCCGACAGAGATGCTGGCGGCGAG 928
721 TGTATAGCTGCGGGGTCACTTGAATCTGACCCGACAGAGATGCTGGCGGCGAG 780
929 AGCGGCTCCGCGGGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCG 988
781 AGCGGCTCCGCGGGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCG 839
989 GTGCGAGGCTCCATCATCACCCGAGTGTGATGTCGACAGCGGCACTGGTGGAAAA 1048
840 GTGCGAGGCTCCATCATCACCCGAGTGTGATGTCGACAGCGGCACTGGTGGAAAA 899
1049 ACCTCTTAACATCCATGGCATTTGACAGGCAATTTGGGGGATTTTGAGCAATCTTTTCA 1108
900 ACCTCTTAACATCCATGGCATTTGACAGGCAATTTGGGGGATTTTGAGCAATCTTTTCA 959
1109 GTTCTATGAGCGGATACCAATGAGAAAAAGTATTTCTCATCAAAATATGATCCAA 1168
960 GTTCTATGAGCGGATACCAATGAGAAAAAGTATTTCTCATCAAAATATGATCCAA 1019
1169 GACCAAGAACATGACATTTGCGCTGATGAGAGCTGCAAGAGCTTGTGACTTCAAGACCT 1228
1020 GACCAAGAACATGACATTTGCGCTGATGAGAGCTGCAAGAGCTTGTGACTTCAAGACCT 1079
1229 AGTGAACACAGTGTGTGTGCGCAACCCAGGCAATGATGCTGCAAGCAAGAACCTGTGCTG 1288

1080 AGTGAACACAGTGTGTGTGCGCAACCCAGGCAATGATGCTGCAAGCAAGACCTTGTG 1139
1289 GATTTCCGGGTGGGGGCGCACCGAGAGAGAAAGAACCTGAGAAAGTGTGTAACGCTGC 1348
1140 GATTTCCGGGTGGGGGCGCACCGAGAGAGAAAGAACCTGAGAAAGTGTGTAACGCTGC 1199
1349 CAAGTGTCTTCATTTGAGACACAGATGCAACAGCAGATATGTCATGACAACTGAT 1408
1200 CAAGTGTCTTCATTTGAGACACAGATGCAACAGCAGATATGTCATGACAACTGAT 1259
1409 CACACAGCAGATGATGTCGCGGCTTCTGTCAGAGGGAACGTCATTTCTTGCAAGGTGA 1468
1260 CACACAGCAGATGATGTCGCGGCTTCTGTCAGAGGGAACGTCATTTCTTGCAAGGTGA 1319
1469 CAGTGAGAGGCTTGTGCTACTTGTGCAAGAAATATGTCGTCATGAGGAGATACAA 1528
1320 CAGTGAGAGGCTTGTGCTACTTGTGCAAGAAATATGTCGTCATGAGGAGATACAA 1379
1529 CTGGGCTTGTGCTGTGCAAGAACTTACAGACAGAGAGTGTACGGGAATGTGATGAT 1588
1380 CTGGGCTTGTGCTGTGCAAGAACTTACAGACAGAGAGTGTACGGGAATGTGATGAT 1439
1589 CACGAGCTGATTTATGCAAAATGAGGCGACAGCGCTAA 1628
1440 CACGAGCTGATTTATGCAAAATGAGGCGACAGCGCTAA 1479

RESULT 5
US-08-807-151-2
Sequence 2, Application US/08807151
Patent No. 6043033
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Applicant: Lal, Preeti
TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,151
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0227 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SCORNIOTI
CLONE: 556016

US-08-807-151-2

Query Match 28.6%; Score 983; DB 3; Length 1077;
Best Local Similarity 99.8%; Pred. No. 3.2e-256;
Matches 994; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

758 AGCGATCCACCACTTTATGAAGTGAACACAGTCCCGCAATGTCATATTA 817
83 AGCGATCCACCACTTTATGAAGTGAACACAGTCCCGCAATGTCATATTA 142
818 AAACGTACACAGTGAAGTCCCTTCAAAAGAGTGTCTTCTTACGCTATAGC 877
143 AAACGTACACAGTGAAGTCCCTTCAAAAGAGTGTGTCTTACGCTATAGC 202
878 TCGCGGCTCAACTTGAATCAAGCCGACAGAGATGCTGGGGGAGAGCGGCTC 937
203 TCGCGGCTCAACTTGAATCAAGCCGACAGAGATGCTGGGGGAGAGCGGCTC 262
938 CCGGGGGCTGGCCCTGGGGCAGTCAAGCTGACATCCAGAACGTCAGTGGGAG 997
263 CCGGGGGCTGGCCCTGGGGCAGTCAAGCTGACATCCAGAACGTCAGTGGGAG 321
998 CTCATCATCAACCCCGAGTGTGACAGCCCGCAGTGTGGGAAACCTCTTAA 1057
322 CTCATCATCAACCCCGAGTGTGACAGCCCGCAGTGTGGGAAACCTCTTAA 381
1058 CAATCATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 1117
382 CAATCATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 441
1118 AGCGGATACCAAGTGAAGAGTATTTCTCATCAATTTGATGATCCAGAACAA 1177
442 AGCGGATACCAAGTGAAGAGTATTTCTCATCAATTTGATGATCCAGAACAA 501
1178 CAATGATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 1237
502 CAATGATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 561
1238 AGTGTGTGCTGACCAAGCAGTGTGACAGCCAGTGTGTGATTTCCGG 1297
562 AGTGTGTGCTGACCAAGCAGTGTGACAGCCAGTGTGTGATTTCCGG 621
1298 GTGGGGGGCCACGAGAGAGAGAGAGTCTGAGAGTGTGAGAGTGTG 1357
622 GTGGGGGGCCACGAGAGAGAGAGTCTGAGAGTGTGAGAGTGTG 681
1358 TCTCATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 1417
682 TCTCATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 741
1418 CATGATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 1477
742 CATGATGATGATGAGAGGATTTGGGGATTTGAGACATCTTTCATGTTATG 801
1478 GCTGTGTGCTGACCAAGCAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 1537
802 GCTGTGTGCTGACCAAGCAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 861
1538 TGGCGTGTGCTGACCAAGCAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 1597
862 TGGCGTGTGCTGACCAAGCAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 921
1598 GATTTATGACAAATGAGAGGAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 1657
922 GATTTATGACAAATGAGAGGAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 981
1658 TTACAAAGAAACAAATGAGAGGAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 1717
982 TTACAAAGAAACAAATGAGAGGAGTGTGACAGCCCGCAGTGTGTGAGAGTGTG 1041
1718 TTACAAAGTGTGATTTTATTTATTAACAGTGTG 1753
1042 TTACAAAGTGTGATTTTATTTATTAACAGTGTG 1077

RESULT 6
US-09-478-957-2
Sequence 2; Application US/09478957
Patent No. 635048

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/478,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,151
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0227 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SCORNOT01
CLONE: 556016
US-09-478-957-2

Query Match 28.6%; Score 983; DB 4; Length 1077;
Best Local Similarity 99.8%; Pred. No. 3.2e-256;
Matches 994; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

758 AGCGATCCACCACTTTATGAAGTGAACACAGTCCCGCAATGTCATATTA 817
83 AGCGATCCACCACTTTATGAAGTGAACACAGTCCCGCAATGTCATATTA 142
818 AAACGTACACAGTGAAGTCCCTTCAAAAGAGTGTCTTCTTACGCTATAGC 877
143 AAACGTACACAGTGAAGTCCCTTCAAAAGAGTGTGTCTTACGCTATAGC 202
878 TCGCGGCTCAACTTGAATCAAGCCGACAGAGATGCTGGGGGAGAGCGGCTC 937
203 TCGCGGCTCAACTTGAATCAAGCCGACAGAGATGCTGGGGGAGAGCGGCTC 262
938 CCGGGGGCTGGCCCTGGGGCAGTCAAGCTGACATCCAGAACGTCAGTGGGAG 997
263 CCGGGGGCTGGCCCTGGGGCAGTCAAGCTGACATCCAGAACGTCAGTGGGAG 321
998 CTCATCATCAACCCCGAGTGTGACAGCCCGCAGTGTGGGAAACCTCTTAA 1057
322 CTCATCATCAACCCCGAGTGTGACAGCCCGCAGTGTGGGAAACCTCTTAA 381

Oy 1058 CAATTCATGCGATTGAGACGGCATTTCGGGGGATTTTGAACAATCTTTCATCTTCTATAG 1117
 Db 382 CAATTCATGCGATTGAGACGGCATTTCGGGGGATTTTGAACAATCTTTCATCTTCTATAG 441
 Oy 1118 AGCCGATACCAAGTAGAAAAAGTAGTTTCTCATTCACAAATATATAGCTCCAAAGCACAAGAA 1177
 Db 442 AGCCGATACCAAGTAGAAAAAGTAGTTTCTCATTCACAAATATATAGCTCCAAAGCACAAGAA 501
 Oy 1238 AGTGTGTCGTGCCCACACCGAGCATGATGTCTGCAGCCAGAACAGCTCTGCTGATTTCCGG 1297
 Db 582 AGTGTGTCGTGCCCACACCGAGCATGATGTCTGCAGCCAGAACAGCTCTGCTGATTTCCGG 621
 Oy 1298 GTGGGGGGGCCACCGAGGAGAAAGGGAAGACCTCAGAAGTGTCTGAACGCTGCCAAGTGTCT 1357
 Db 622 GTGGGGGGGCCACCGAGGAGAAAGGGAAGACCTCAGAAGTGTCTGAACGCTGCCAAGTGTCT 681
 Oy 1358 TCTCATTTGAGACACAGAGATGCAACAGACAGATATGTCTATGACAACTGTATCACAACAGC 1417
 Db 682 TCTCATTTGAGACACAGAGATGCAACAGACAGATATGTCTATGACAACTGTATCACAACAGC 741
 Oy 1418 CATGATGTGTCGCCGGCTCTCTGACAGGGGAACGTCATCTTGCCAGGGGGAACAGTAGAGG 1477
 Db 742 CATGATGTGTCGCCGGCTCTCTGACAGGGGAACGTCATCTTGCCAGGGGGAACAGTAGAGG 801
 Oy 1478 GCGCTGTGCTCATCTTCCGAAGCAATATCTGTGTGCTGATAGGGGATACAAAGCTGGGGTTC 1537
 Db 802 GCGCTGTGCTCATCTTCCGAAGCAATATCTGTGTGCTGATAGGGGATACAAAGCTGGGGTTC 861
 Oy 1538 TGGCTGTGCCAAAGCTTACAGACACAGAGAGTGTACGGGAATGTGATGTGATTTACACGAGCTG 1597
 Db 862 TGGCTGTGCCAAAGCTTACAGACACAGAGAGTGTACGGGAATGTGATGTGATTTACACGAGCTG 921
 Oy 1598 GATTATACGCAAAATGAGGGCAGACGGCTATACCAATAGGTCTTGCTCTTACGCTGCT 1657
 Db 922 GATTATACGCAAAATGAGGGCAGACGGCTATACCAATAGGTCTTGCTCTTACGCTGCT 981
 Oy 1658 TTACAGAAAAAACAATGAGGGCGCTGTTTGTCTTCCCGTCGATGATTTACTCTTAGAGATGA 1717
 Db 982 TTACAGAAAAAACAATGAGGGCGCTGTTTGTCTTCCCGTCGATGATTTACTCTTAGAGATGA 1041
 Oy 1718 TTTCAGAGGTCACTTCATTTTATTTAAACAGTGAAT 1753
 Db 1042 TTTCAGAGGTCACTTCATTTTATTTAAACAGTGAAT 1077
 RESULT 7
 US-09-605-785-384
 Sequence 384, Application US-09-605785
 Patent No. 6321716.
 GENERAL INFORMATION:
 APPLICANT: Xu, Jifengchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yiqui
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick L.
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skelky, Yasir A.W.
 APPLICANT: Hepler, William
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

```

1 FILE REFERENCE: 210121.427C16
2 CURRENT APPLICATION NUMBER: US/09/605,785
3 CURRENT FILING DATE: 2000-06-27
4 NUMBER OF SEQ ID NOS: 835
5 SOFTWARE: FASTSeq for Windows Version 3.0
6 SEQ ID NO 384
7 LENGTH: 557
8 TYPE: DNA
9 ORGANISM: Homo sapiens
10 US-09-605-785-384
11
12 Query Match 14.2% Score 490; DB 4; Length 557;
13 Best Local Similarity 98.0%; Pred. No. 6,2e-123;
14 Matches 496; Conservative 0; Mismatches 10; Indels 0; Gaps 0
15
16 QY 2717 AAAGTCCCATGCTGGCGCGAAGAAAGATGTGTTTGTGGACCTCTGTGG 2776
17 Db 32 AAATTCGGGGCGCGCTCGACGAAAGAAAGATGTGTTTGTGGACCTCTGTGG 2776
18 QY 2777 TCCCTTCCAATGCTGTGGGTTTCCAACACAGGGGAAAGGTCCTTTTGCAATGCCAATGTC 2836
19 Db 92 TCCCTTCCAATGCTGTGGGTTTCCAACACAGGGGAAAGGTCCTTTTGCAATGCCAATGTC 2836
20 QY 2837 CATATCCATGAGCATACTACTACATGCTGCTCCGCGCAGACGAGGCTGTTTGA 2896
21 Db 152 CATATCCATGAGCATACTACTACATGCTGCTCCGCGCAGACGAGGCTGTTTGA 2896
22 QY 2897 AGAATGAATGATGATTTCTACAGCTAGGACTTAACCTTGAATGGAAGTCTTCCATC 2956
23 Db 212 AGAATGAATGATGATTTCTACAGCTAGGACTTAACCTTGAATGGAAGTCTTCCATC 2956
24 QY 2957 CCATTTCGACGATCCGCTGTGTCACATGCTCTGTAGAGACGACATTTCCAGGACCTT 3016
25 Db 272 CCATTTCGACGATCCGCTGTGTCACATGCTCTGTAGAGACGACATTTCCAGGACCTT 3016
26 QY 3017 GGAACACATTGGCATACTGTAAAGTGTGCTGCCCAAGACACATCTTAAAGGTGTTGTA 3076
27 Db 332 GGAACACATTGGCATACTGTAAAGTGTGCTGCCCAAGACACATCTTAAAGGTGTTGTA 3076
28 QY 3077 TGGTGAAGAACGCTCTCTCTTATTTATGGCCCTCTTATTTATGTGAACAACTGTTGGTCT 3136
29 Db 392 TGGTGAAGAACGCTCTCTCTTATTTATGGCCCTCTTATTTATGTGAACAACTGTTGGTCT 451
30 QY 3137 TTTTGTGATCTTTTAACTGTAAGTCTAATGTGTAAGTGAATATCATGCAATTA 3196
31 Db 452 TTTTGTGATCTTTTAACTGTAAGTCTAATGTGTAAGTGAATATCATGCAATTA 511
32 QY 3197 ATTATGCGATTTTTCCTCAAGTAA 3222
33 Db 512 ATTATGCGATTTTTCCTCAAGTAA 537
34
35 RESULT 8
36 US-09-439-313-384
37 Sequence 384, Application US/09439313
38 Patent No. 6329505
39 GENERAL INFORMATION:
40 APPLICANT: Xu, Jiangchun
41 APPLICANT: Dillon, Davin C.
42 APPLICANT: Mitcham, Jennifer L.
43 APPLICANT: Harlocker, Susan Louise
44 APPLICANT: Jiang Yugu
45 APPLICANT: Reed, Steven G.
46 APPLICANT: Kalos, Michael
47 APPLICANT: Fanger, Gary
48 APPLICANT: Retter, Mark
49 APPLICANT: Solk, John
50 APPLICANT: Day, Craig
51 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
52 FILE REFERENCE: 210121.427C9
53 CURRENT APPLICATION NUMBER: US/09/439,313
54 CURRENT FILING DATE: 1999-11-12

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Db 301 GTCCTTTTGCATGCGCAATGCGCAATACCATGACGACTACGCTACCATGTTCTGCTTC 360
Qy 2874 CTGGCCACAGCAGCGTGGTTTGCAGAAATGAATGAATGAT 2913
Db 361 CTGGCCACAGCAGCGTGGTTTGCAGAAATGAATGAATGAT 400
RESULT 13
US-09-232-149A-325
; Sequence 325, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 325
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-325
Query Match 11.6%; Score 398.4; DB 4; Length 400;
Best Local Similarity 99.8%; Pred. No. 3.2e-98;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2514 ACAGTGTTCACATGTTATGTTTCTACACATGCTACCTGAGTCCCTGGAACCTAGCT 2573
Db 1 ACAGTGTTCACATGTTATGTTTCTACACATGCTACCTGAGTCCCTGGAACCTAGCT 60
Qy 2574 TTTGATGTCTCCAGTAGTCACACCTTCATTTAACTTTTGAACCTGATATCTTTGCCA 2633
Db 61 TTTGATGTCTCCAGTAGTCACACCTTCATTTAACTTTTGAACCTGATATCTTTGCCA 120
Qy 2634 AGTAAGAGTGTGGGCTTATTTGAGTGTGCTTTCACAAATGACTGGCTCCGACTTAAGT 2693
Db 121 AGTAAGAGTGTGGGCTTATTTGAGTGTGCTTTCACAAATGACTGGCTCCGACTTAAGT 180
Qy 2694 TCTATTAATGAATGTGCTGAGCAAGCAAGTCCCATGCTGCGGCGGAGAGAGAAATGT 2753
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RESULT 14
US-09-605-785-401
; Sequence 401, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 401
LENGTH: 355
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(355)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-401
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Best Local Similarity 99.2%; Pred. No. 1.1e-85;
Matches 352; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 121 TAAGAGTGTGGGCTTATTTGAGTGTGCTTTCACAAATGACTGGCTCCGACTTAAGT 180
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Db 301 CCCTTTTGCATGCGCAATGCGCAATACCATGACGACTACCTACCATGTTCTGCTTC 360
RESULT 15
US-09-439-313-401
; Sequence 401, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig

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; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427c9
; CURRENT APPLICATION NUMBER: US/09/439.313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 401
; LENGTH: 355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(355)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-401
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Query Match          10.28; Score 352; DB 4; Length 355;
Best Local Similarity 99.28; Pred. No. 1.1e-85;
Matches 352; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2636 TAAGAGTGCGCTATTTGAGCTGCTTGACAAAATGAGCTGCTCCGACTTACGTTTC 2695
      |||||||
Db 121 TAAGAGTGCGCTATTTGAGCTGCTTGACAAAATGAGCTGCTCCGACTTACGTTTC 180

QY 2696 TATAAATGATGTGCTGAGCAAAAGTGCCCATGTGTGGCGGCAAGAGAAAGATGTGT 2755
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Search completed: January 16, 2003, 08:15:11
Job time : 145 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 17:52:41 ; Search time 4199 Seconds
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Title: US-09-807-201-8

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

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18: em_gss_hum:*
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25: em_gss_other:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1551.6	45.1	2394	11	AF318374 Homo sapi
2	782.6	22.7	866	13	BI761763 603046751
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4	647.2	18.8	909	12	BG485061 602503876
5	626.4	16.2	639	14	BM784118 K-EST0062
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9	553	16.1	553	13	BM126575
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ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATUERS
1	AF318374	Homo sapiens pp9284 mRNA, complete cds.	AF318374	GI:18027839	HTC.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 2394)	Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.	Novel human cDNA clones with function of inhibiting cancer cell growth	Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China	source
2	AF318374	Homo sapiens pp9284 mRNA, complete cds.	AF318374	GI:18027839	HTC.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	2 (bases 1 to 2394)	Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.	Novel human cDNA clones with function of inhibiting cancer cell growth	Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China	source
3	AF318374	Homo sapiens pp9284 mRNA, complete cds.	AF318374	GI:18027839	HTC.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	3 (bases 1 to 2394)	Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.	Novel human cDNA clones with function of inhibiting cancer cell growth	Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China	source
4	AF318374	Homo sapiens pp9284 mRNA, complete cds.	AF318374	GI:18027839	HTC.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	4 (bases 1 to 2394)	Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.	Novel human cDNA clones with function of inhibiting cancer cell growth	Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China	source
5	AF318374	Homo sapiens pp9284 mRNA, complete cds.	AF318374	GI:18027839	HTC.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	5 (bases 1 to 2394)	Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.	Novel human cDNA clones with function of inhibiting cancer cell growth	Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China	source
6	AF318374	Homo sapiens pp9284 mRNA, complete cds.	AF318374	GI:18027839	HTC.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	6 (bases 1 to 2394)	Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.	Novel human cDNA clones with function of inhibiting cancer cell growth	Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China	source

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Query Match 45.1%; Score 1551.6; DB 11; Length 2394;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 4; Indels 5; Gaps 4;

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OY 1676 GCTGCTTTTGTCTCCCGGTCATGATTTACTGTAGAGATGATTCAGAGGTCATTCANT 1735.
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Db 1054 CTGGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1113

OY 2036 CTGACAGGGCTG-CCTCTGGGGCCACTTGGTGTGCTCCAGCTTACCTCTCCACAAAGG 2094
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OY 2095 GATTTTGTGATGAGGTTCTTAGAGCTTACAGCCCTGAGCTGATGATGATGATGATGATG 2154
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KEYWORDS B1761763.1 GI:15733341
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ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 866)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
<http://image.liml.gov>
 Plate: LIML1467 row: e column: 13
 High quality sequence stop: 781.

FEATURES

source

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 oligo-dr primed and directionally cloned (EcoRV site is
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 enriched for full-length clones and was constructed by C.
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ORIGIN

Query Match

Best Local Similarity 96.1%; Score 782.6; DB 13; Length 866;

Matches 835; Conservative 0; Mismatches 29; Indels 5; Gaps 3;

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 Db 421 GCTGCGCTACTGTGAAGTTGATGGGACGAGTGTCTCAACTCTGGGATAGATGGAC 480
 QY 512 TCTCAGGTAACCTGCATCAACCCCTTAATGATGATGGCGTGTACACTGCCCGGC 571
 Db 481 TCTCAGGTAACCTGCATCAACCCCTTAATGATGATGGCGTGTACACTGCCCGGC 540
 QY 572 GGGAGAGAGAGATGGTGTGCTTACGAGCAAACTTCACTTCAAGTGTAC 631
 Db 541 GGGAGAGAGAGATGGTGTGCTTACGAGCAAACTTCACTTCAAGTGTAC 600
 QY 632 TCATCTCAGAGAGATGCTTGGACCCCTGTGTGCCAAGACGATGGAACGAACTACGGG 691

Db 601 TCATCTCAGAGAGATGCTTGGACCCCTGTGTGCCAAGACGAGCAACGAACTACGGG 660
 QY 692 CCGGCGCCCTGCAGGAGCATGGCTATTAAGATAATTTTACTCTGTGCCAAGATAGTG 751
 Db 661 CCGGCGCCCTGCAGGAGCATGGCTATTAAGATAATTTTACTCTGTGCCAAGATAGTG 720
 QY 752 GATGACAGCGGATCCA-CCAGCTTTATGAACGTGAACACAGTGGCGCAATGCTGATAT 810
 Db 721 GATGACAGCGGATCCAACCGCTTTATGAACGTGAACACAGTGGCGCAATGCTGATAT 780
 QY 811 CTATTAATAAAGCTGTACACAGTATGCTGTCTTCAAAAAGCAGTGGTCTTTACGCT- 869
 Db 781 CTATTAATAAAGCTGTACAGTAAAGCTGTG---TTCTCATTAAGCAGGAGGTTCTGTACCCG 837
 QY 870 GTATAGCTTGGGGGTCACTGATACCA 898
 Db 838 GTTATCTGGCGGGTCACTGATACCA 866

RESULT 3

BM784096 725 bp mRNA linear EST 05-MAR-2002

LOCUS K-EST0062160 S7SNU719 Homo sapiens cDNA clone S7SNU719-31-D03 5',

DEFINITION mRNA sequence.

ACCESSION BM784096

VERSION BM784096.1 GI:19132328

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 725)

REFERENCE Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

UNPUBLISHED

CONTACT: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4470

Email: yongsung@mail.kr.ibm.re.kr

Plate: 31 row: D column: 03

High quality sequence stop: 725.

FEATURES

source

1. .725

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1b="S7SNU719-31-D03"

/clone_11b="S7SNU719"

/sex="M"

/tissue_type="Stomach"

/cell_type="Epithelial"

/cell_line="SNU-719"

/lab_host="top10F"

/note="Organ: Stomach; Vector: pCNS; Site.1: EcoRI;

Site.2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated

with tabacco acid pyrophosphatase (TAP). The dephosphorylated

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

BASE COUNT 168 a 177 c 204 g 176 t
ORIGIN full-length enriched cDNA library.

Query Match 20.0%; Score 688.4; DB 1.4; Length 725;
Best Local Similarity 99.4%; Pred. No. 2e-148; Indels 3; Gaps 3;
Matches 722; Conservative 0; Mismatches 1;

1158 TATGACTCCAAAGACCAAGAAACAATGACATGGCGCTGATGAAAGCTGACAGAACCTCTGACT 1217
1 TATGACTCCAAAGACCAAGAAACAATGACATGGCGCTGATGAAAGCTGACAGAACCTCTGACT 60
1218 TTCAACGACCTTGTGTAACCACTGTGTCTGCCAACCCAGGATGATGCTGACAGCCAGAA 1277
61 TTCAACGACCTTGTGTAACCACTGTGTCTGCCAACCCAGGATGATGCTGACAGCCAGAA 120
1278 CAGCTCTGTGATTTCCGGGCGGGGGGCGACGAGGAGAAAGGGAAGCTCAGCAAGT 1337
121 CAGCTCTGTGATTTCCGGGCGGGGGGCGACGAGGAGAAAGGGAAGCTCAGCAAGT 180
1338 CTGAACGCTGCGCAAGGCTGCTCTCATTTGAGACACAGAGATGCAAGACGAGATATGCTAT 1397
181 CTGAACGCTGCGCAAGGCTGCTCTCATTTGAGACACAGAGATGCAAGACGAGATATGCTAT 240
1398 GACAACTGATACACACACAGCCATGATCTGTGCGCGCTTCTCTGAGGGGAACTGATCT 1457
241 GACAACTGATACACACAGCCATGATCTGTGCGCGCTTCTCTGAGGGGAACTGATCT 300
1458 TGGCAGGGGAGAGTGGAGGGGCTGCGGCTGATGAGAAACAATATCTGTGTGCTGATA 1517
301 TGGCAGGGGAGAGTGGAGGGGCTGCGGCTGATGAGAAACAATATCTGTGTGCTGATA 359
1518 GGGGATACACAGCTGGGGTCTGTGCTGCGCAAGCTTACAGACCAAGAGTGTACGGGAAT 1577
360 GGGGATACACAGCTGGGGTCTGTGCTGCGCAAGCTTACAGACCAAGAGTGTACGGGAAT 419
1578 GTGATGATTTACAGAGCTGATTTATGACAAATGAGGGGAGACGGCTATATCCACATGG 1637
420 GTGATGATTTACAGAGCTGATTTATGACAAATGAGGGGAGACGGCTATATCCACATGG 479
1638 TCTTGCTGCTGAGCGCTGTTCACAAAGAAACAAT-GGGGCGGTGTTGCTTCCCGCTGC 1696
480 TCTTGCTGCTGAGCGCTGTTCACAAAGAAACAATGAGGGGAGTGTGCTTCCCGCTGC 539
1697 ATGATTTACTCTTACAGATGATTTACAGAGCTCACTTATTTATTAACAGTGAATCTGT 1756
540 ATGATTTACTCTTACAGATGATTTACAGAGCTCACTTATTTATTAACAGTGAATCTGT 599
1757 CTGGCTTTGGCACTCTCTGCAATTTCTGTGACAGGCTGACAGTGGCTCCCTGCCAGCTGC 1816
600 CTGGCTTTGGCACTCTCTGCAATTTCTGTGACAGGCTGACAGTGGCTCCCTGCCAGCTGC 659
1817 TCTCCCTAACCCCTTGTCCGCAAGGGGAGTGGCCGGC-TGGTTTGGGCACTGGCGGTG 1875
660 TCTCCCTAACCCCTTGTCCGCAAGGGGAGTGGCCGGC-TGGTTTGGGCACTGGCGGTG 719
1876 AAGTGT 1881
720 AAGTGT 725

RESULT 4
LOCUS BG485061 909 bp mRNA linear EST 21-MAR-2001
DEFINITION 602503876P1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4617283 5',
mRNA sequence.
ACCESSION BG485061
VERSION BG485061.1 GI:13417340
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 909)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Clontech Laboratories, Inc.
CDNA Library Preparation: Clontech Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMUL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMUL at:
<http://image.lnl.gov>
Plate: LICM1373 row: h column: 20
High quality sequence stop: 747.

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:4617283"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (99cgcctcggcc); Site: 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATGATGCG-3' and 3' adaptor sequence:
5'-ATTCAGAGCGCGGAGGGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH-MGC Library."

BASE COUNT 205 a 207 c 259 g 228 t
ORIGIN

Query Match 18.8%; Score 647.2; DB 1.2; Length 909;
Best Local Similarity 90.9%; Pred. No. 7.1e-139;
Matches 811; Conservative 0; Mismatches 68; Indels 13; Gaps 11;

1987 CTTGAGATGAAGAAAGACAGACATGGAAGGAGAGACCGAGCTGCGACCGCGGCT 2046
2 CTTGAGATGAAGAAAGACAGACATGGAAGGAGAGACCGAGCTGCGACCGCGGCT 61
2047 G-CCTGTGGGGCACTTGATGTGCCAGCGCTCTCCACAAAGGGAATTTGTCTGA 2105
62 GCCCTCTGGGGCACTTGATGTGCCAGCGCTCTCCACAAAGGGAATTTGTCTGA 121
2106 TGGTTCTTGAAGCTTACAGACCTGTGATGTTGCCAGAAATTAAGGACCAAGCTTC 2165
122 TGGTTCTTGAAGCTTACAGACCTGTGATGTTGCCAGAAATTAAGGACCAAGCTTC 181
2166 ATGGGTGGACCGCTGTGATGTTGCCAGAAATTAAGGGAAGAAACATTTTGTCTATGG 2225
182 ATGGGTGGAGCTGTGATGTTGCCAGAAATTAAGGGAAGAAACATTTTGTCTATGG 240
2226 GTGAGAAATATAGACAGTCCCTTGGGTGAGAGGAAGAAATTAAGGAACTTGGCTG 2285
241 GTGAGAAATATAGACAGTCCCTTGGGTGAGAGGAAGAAATTAAGGAACTTGGCTG 299
2286 AGCACTCTGTGAGCTGTCCACCTGTGACATTTGGTGGGCTCTGGAGGAGACTCA 2345
300 AGCACTCTGTGAGCTGTCCACCTGTGACATTTGGTGGGCTCTGGAGGAGACTCA 359
2346 GCGTTCCTCCTATCTCTCTGACAGCTCTCTGTACACCTGTGAGAGTGCACATGCCCT 2405
360 GCGTTCCTCCTATCTCTCTGACAGCTCTCTGTACACCTGTGAGAGTGCACATGCCCT 419
2406 TGGTCTGTGGAGGGGCGCAAGTGTGGCACACATTTGGCTCTGAGGCTGTGATGCA 2465
420 TGGTCTGTGGAGGGGCGCAAGTGTGGCACACATTTGGCTCTGAGGCTGTGATGCA 479
2466 CTGGAATTTAGAGTCCATGGGGGAATCAGGATGCTCAGTTTAAAGTACATGTTTCA 2525

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Db 480 CTGGAAATTGAGTCCATGGGGAAATCAAGATGCTCAGTTTAAGCTACACTGTTTCCA 539
Oy 2526 TGTATGTTTACACATGCTACCTCAGTGTCTCTGGAACCTTTGATGTCTCC 2585
Db 540 TGTATGTTTACACATGCTACCTCAGTGTCTCTGGAACCTTTGATGTCTCC 598
Oy 2586 AAGTACTCCACC-TTCATTTTAAGTCTTTGAAGTGTATCATCTTTGCCAAGTAAGAGTGG 2644
Db 599 AAGTACTCCACCCTTTCATTTTAAGTCTTTGAAGTGTATCATCTTTGCCAAGTAAGAGTGG 658
Oy 2645 TGGCCATTTCAGCTGCTTTGACAAATGATGCTGCTCAGCTTAAGCTTTAAATGA 2704
Db 659 TGGGCTATTTCAGCTGCTTTGACAAATGATGCTG-TCTGACTTA--CGCTATAAATGA 715
Oy 2705 AAGTGTGGAAGCAAGTGGCCATGCTGGGCGGAGAGAAAGATGTTTGTGTTTG 2764
Db 716 AAGTGT-TGAAGCAAGTGGCCATGCTGGGCGGAGAGAAAGATGTTTGTGTTTG 773
Oy 2765 GACTCTCTGTGCTCCCTTCATGCTGTGGGTTTCCACAGGAGGAGGCTCCCTTTGCG 2824
Db 774 GACTCTCTGTGCTCCCTTCATGCTGTGGGTTTCCAC--AGGGAGAGGCTCCCTTTGCG 830
Oy 2825 ATTGCCAAGTGGCATACCATGAGCACTACTACCATGCTGCTGCTCTG 2876
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RESULT 5
BM784118 639 bp mRNA linear EST 05-MAR-2002
LOCUS BM784118
DEFINITION K-HST0062185 S7SNU719 Homo sapiens cDNA clone S7SNU719-31-F04 5',
mRNA sequence.
ACCESSION BM784118
VERSION BM784118.1 GI:19132350
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 639)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 31 row: F column: 04
High quality sequence stop: 639.
Location/Qualifiers
1..639
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="S7SNU719-31-F04"
/clone_id="S7SNU719"
/sex="M"
/tissue_type="Stomach"
/cell_type="Epithelial"
/cell_line="SND-719"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pONS; Site:1; EcoRI;
Site:2; NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was

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adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okazaki-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

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BASE COUNT 159 a 148 c 176 g 156 t
ORIGIN
Query Match 18.2%; Score 626.4; DB 14; Length 639;
Best Local Similarity 99.7%; Pred. No. 4,4e-134;
Matches 638; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Oy 1158 TATGATCCCAAGCAAGAAATGATGATGCTGCTGTAAGTGTGAGAAAGCTCTGACT 1217
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Oy 1218 TTCAAGACCTAGTGAAGCAAGTGTGTGCTGCTGCAAGCAAGCAAGTGTGAGCAAG 1277
Db 61 TTCAAGACCTAGTGAAGCAAGTGTGTGCTGCTGCAAGCAAGCAAGTGTGAGCAAG 120
Oy 1278 CAGCTGTGCTGGAATTTCCGGGTGGGGCCACCGAGAGAAAGGAAAGCTGAGAGTG 1337
Db 121 CAGCTGTGCTGGAATTTCCGGGTGGGGCCACCGAGAGAAAGGAAAGCTGAGAGTG 180
Oy 1338 CTGACGCTGCAAGGAGGCTCTCATTTGAGACACAGAGATGCAAGCAAGCAAGTATGCTAT 1397
Db 181 CTGACGCTGCAAGGAGGCTCTCATTTGAGACACAGAGATGCAAGCAAGCAAGTATGCTAT 240
Oy 1398 GACACCTGATCAACACAGCATGATGTGCCGCTCTCTGCAAGGAGGAAAGCTGATTC 1457
Db 241 GACACCTGATCAACACAGCATGATGTGCCGCTCTCTGCAAGGAGGAAAGCTGATTC 300
Oy 1458 TGGCAGGCTGACAGTGGAGGGCTCTGCTGCTTCCAGCAAGCAAGTGTGCTGATTA 1517
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Oy 1518 GGGGATACAAAGCTGGGGGTTTGCTGCTGCTGCAAGGCTTACAGCAGAGAGTACGGGAAT 1577
Db 360 GGGGATACAAAGCTGGGGGTTTGCTGCTGCTGCAAGGCTTACAGCAGAGAGTACGGGAAT 419
Oy 1578 GTGATGATTCACAGCAAGTGTATTCGACAAATGAGGAGCAGACGGCTATTCACATGG 1637
Db 420 GTGATGATTCACAGCAAGTGTATTCGACAAATGAGGAGCAGACGGCTATTCACATGG 479
Oy 1638 TCTTCTGCTGTGACGTCGTTTACAAAGAAACATGGGCTGTTTCTCCCGTGCA 1697
Db 480 TCTTCTGCTGTGACGTCGTTTACAAAGAAACATGGGCTGTTTCTCCCGTGCA 539
Oy 1698 TGATTTACTCTTGAAGTGAAGTATTCAGAGGCTCACTTATTTATTAACAGTGAAGTTC 1757
Db 540 TGATTTACTCTTGAAGTGAAGTATTCAGAGGCTCACTTATTTATTAACAGTGAAGTTC 599
Oy 1758 TGGCTTTGGCAGCTCTGCAATTCCTGTGCAAGGCTGCAGTG 1797
Db 600 TGGCTTTGGCAGCTCTGCAATTCCTGTGCAAGGCTGCAGTG 639

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RESULT 6
BE867224 792 bp mRNA linear EST 20-OCT-2000
LOCUS BE867224
DEFINITION 601442284F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846572 5',
mRNA sequence.
ACCESSION BE867224
VERSION BE867224.1 GI:10316000
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 792)

```

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov

Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM9559 row: g column: 21
 High quality sequence stop: 676.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
 /clone_1db="NIH_MGC_65"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: colon; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."
 BASE COUNT 161 a 202 c 244 g 185 t
 ORIGIN

Query Match 16.9%; Score 583.2; DB 12; Length 792;
 Best Local Similarity 98.8%; Pred. No. 4.5e-124;

Matches 640; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

OY 1762 TTTGGACATCTCTGCGATTCGTGAGCGTGCAGTGGCTCCCTCCAGCCTGCTCTCC 1821

DB 1 TTTGGACATCTCTGCGATTCGTGAGCGTGCAGTGGCTCCCTCCAGCCTGCTCTCC 60

OY 1822 CTAAACCCCTTGTCCGCAAGGGGTGATGGCGGGTGTGTGGGCACTGGCGGTCAAGTGT 1881

DB 61 CTAAACCCCTTGTCCGCAAGGGGTGATGGCGGGTGTGTGGGCACTGGCGGTCAAGTGT 120

OY 1882 GGAGAGAGGGGTGGAGGCTGCCCATGAGATCTTCTCTGCTGACTCTTTCAGAGGGCC 1941

DB 121 GGAGAGAGGGGTGGAGGCTGCCCATGAGATCTTCTCTGCTGACTCTTTCAGAGGGCC 180

OY 1942 AATTTTGGATGAGCATGTGAGCTGTCACTCTCAGCTGATGATGAGATGAAAAAG 2001

DB 181 AATTTTGGATGAGCATGTGAGCTGTCACTCTCAGCTGATGATGAGATGAAAAAG 240

OY 2002 GAGAGACATGGAAGGAGAGACAGCCAGGTGGCAGCTGCAGCGGCTG-CCTCTGGGGCCAC 2060

DB 241 GAGAGACATGGAAGGAGAGACAGCCAGGTGGCAGCTGCAGCGGCTGCGCCCTGGGGCCAC 300

OY 2061 TTGGTAGTGTCCCGCAGCTACTCTCCACAAAGGGATTTTGTGATGGGTTCTTAGAGCC 2120

DB 301 TTGGTAGTGTCCCGCAGCTACTCTCCACAAAGGGATTTTGTGATGGGTTCTTAGAGCC 360

OY 2121 TTAGCAGCCCTGGATGTGGCCAGAAATAAAGGACACAGCCCTTATGGTGGTGAACGTC 2180

DB 361 TTAGCAGCCCTGGATGTGGCCAGAAATAAAGGACACAGCCCTTATGGTGGTGAACGTC 420

OY 2181 GTATGACCTTGTAAAGGGAAACAAACATTTTGTCTTATGGGGTGAATATAGACA 2240

DB 421 GTATGACCTTGTAAAGGGAAACAAACATTTTGTCTTATGGGGTGAATATAGACA 478

OY 2241 GTGCCCCCTGGGTGCGAGGAAGCAATTGAAAAAGAACTTGGCTTAGACACTCTCTGTGCA 2300

DB 479 GTGCCCCCTGGGTGCGAGGAAGCAATTGAAAAAGAACTTGGCTTAGACACTCTCTGTGCA 537

OY 2301 GGTCTCCACCTGACATTTGGTGGGCTCTCTGGAGAGG-AGACTGAGCCTTCTCTCTCAT 2359

DB 538 GGTCTCCACCTGACATTTGGTGGGCTCTCTGGAGAGGAGACTGAGCCTTCTCTCTCAT 597

OY 2360 CTTCCCTGACCTGCTCTAGCACCTTGAGAGTGCACATGCCCTTG 2407

DB 598 CTTCCCTGACCTGCTCTAGCACCTTGAGAGTGCACATGCCCTTG 645

RESULT 7

LOCUS

DEFINITION

BM747154 591 bp mRNA linear EST 04-MAR-2002
 K-ST0021659 S6SNU620 Homo sapiens cDNA clone S6SNU620-20-F02 5',
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 20 row: F column: 02
 High quality sequence stop: 591.
 Location/Qualifiers

FEATURES

source

1..591

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="S6SNU620-20-F02"

/clone_1db="S6SNU620"

/sex="F"

/tissue_type="Ascites"

/cell_type="Scattering floating"

/cell_line="SNU-620"

/lab_host="Top10F"

/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then dephosphorylated
 with tobacco acid pyrophosphatase (TAP). The dephosphorylated
 intact mRNA was ligated with DNA-RNA linker including EcoRI
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

BASE COUNT 153 a 154 c 160 g 124 t
 ORIGIN

Query Match 16.8%; Score 578.4; DB 14; Length 591;
 Best Local Similarity 99.7%; Pred. No. 5.5e-123;

Matches 590; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 817 AAAAAGTACACAGTGTATGCTGTCTTCAAAAAGCACTGTTTCTTACGCTGTATAGC 876

DB 1 AAAAAGTACACAGTGTATGCTGTCTTCAAAAAGCACTGTTTCTTACGCTGTATAGC 60

OY 877 CTGCGGGGTGCACTTGAAGCTCAAGCCGCGAGAGAGATCGTGGGCGCGAGAGCGCCCT 936

DB 61 CTGCGGGGTGCACTTGAAGCTCAAGCCGCGAGAGAGATCGTGGGCGCGAGAGCGCCCT 120

OY	937	CCGGGGGCGTGGCCCTGGGGAGGTCACGCTCCAGCTCCAGAAAGCTCCACGCTGGGGG	996
Db	121	CCCGGGGGCGTGGCCCTGGGGAGGTCACGCTCCAGCTCCAGAAAGCTCCACGCTGGGGG	179
OY	997	GCTCCATCATCACCCCGAGTGGATCGTACAGCCGCCACACTCGCTGGAAAAACCTCTTA	1056
Db	180	GCTCCATCATCACCCCGAGTGGATCGTACAGCCGCCACACTCGCTGGAAAAACCTCTTA	239
OY	1057	ACAATCCATGGCATTTGGACGGCATTTGGGGGATTTTGGACAACTTTTCAATGTTCTATG	1116
Db	240	ACAATCCATGGCATTTGGACGGCATTTGGGGGATTTTGGACAACTTTTCAATGTTCTATG	299
OY	1117	GAGCCGATACCAAGTAAAAAAAGATTTTCATCTCCAAATATGATCTCCAGACCACA	1176
Db	300	GAGCCGATACCAAGTAAAAAAAGATTTTCATCTCCAAATATGATCTCCAGACCACA	359
OY	1177	ACAATGACATTTGCGCTGATGAACTGTCAAGAAAGCTCTGACTTTTCAACGACCTAGTGAAC	1236
Db	360	ACAATGACATTTGCGCTGATGAACTGTCAAGAAAGCTCTGACTTTTCAACGACCTAGTGAAC	419
OY	1237	CAGATGCTCTGCCCAACCCAGGCATGATGCTGCACCCAGAAAGGCTGCTGGATTTTCCG	1296
Db	420	CAGATGCTCTGCCCAACCCAGGCATGATGCTGCACCCAGAAAGGCTGCTGGATTTTCCG	479
OY	1297	GGTGGGGGGCCACCGAGAGAAAGGGAAGACCTCAGAAGTGTCTGAAGCGCTGCCAAGTTC	1356
Db	480	GGTGGGGGGGGCCACCGAGAGAAAGGGAAGACCTCAGAAGTGTCTGAAGCGCTGCCAAGTTC	539
OY	1357	TTTCATATTGAACACACAGAGATGCCACACGACATATGCTATATACAAACCTGAT	1408
Db	540	TTTCATATTGAACACACAGAGATGCCACACGACATATGCTATATACAAACCTGAT	591

RESULT 8	639 bp	mRNA	linear	EST_02-SEP-2001
AI989307				
LOCUS	AI989307 36 prostate cancer cell line LNCaP Homo sapiens cDNA, mRNA			
DEFINITION	AI989307 36 prostate cancer cell line LNCaP Homo sapiens cDNA, mRNA			
ACCESSION	AI989307			
VERSION	AI989307.1			
KEYWORDS	GI:15421055			
SOURCE	EST.			
	human,			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 639)		
	Zhang, J. S. and Smith, D. I.	High throughput screening for androgen regulated genes in LNCap cells: Identification of hA6-2 as an androgen regulated gene over expressed in prostate adenocarcinoma		
	Unpublished (1999)			
	Contact: Zhang, Jin-San			

Dept. Pathology and Lab Medicine
 Mayo Clinic Cancer Center
 200 1st St. SW, Rochester MN 55905, USA
 Tel: 507-2660311
 Fax: 507-2665193
 Email: zhang.jinsan@mayo.edu.
 Location/Qualifiers

```

SOURCE
1. 639
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="prostate cancer cell line LNCap"
/cell_line="LNCap"
/ncbi="prostate cancer metastasized to lymph node;
subtracted cDNA libraries from prostate cancer cell
line LNCap treated with androgen."
BASE COUNT
138 a 146 c 182 g 163 t 10 others
ORIGIN

```

Query Match	16.58;	Score 568.4;	DB 9;	Length 639;
Best Local Similarity	95.08;	Pred. No. 1.1e-120;		

Matches	603:	Conservative	0:	Mismatches	30:	Indels	2:	Gaps	2:
QY	1573	GGATATGATATGATATTCACGAGCTGATTTATTCACAAATGAGGCGACAGCGCTAATCC							1632
Db	1	GGAAATGATATGATATTCACGAGCTGATTTATTCACAAATGAGGCGACAGCGCTAATCCG							60
QY	1693	CATGCTCTGCTCCCTGACGCTGCTTTTCAAGAAACATGGGCGTGGTTTGGTTCCCC							1692
Db	61	CATGCTCTGCTCCCTGACGCTGCTTTTCAAGAAACATGGGCGTGGTTTGGTTCCCC							120
QY	1693	GTGCAATGATTTACTCTTGTAGATGATTTAGAGAGTCACTTCATTTTATTTAAACAGTGAAC							1752
Db	121	GTGCATATGTTTACTCTTGTAGATGATTTAGAGAGTCACTTCATTTTATTTAAACAGTGAAC							180
QY	1753	TTGTCTGGCTTTTGGCACTCTCTGCCATTTCTGTGACGCTGACAGTGGCTCCCTGCCAGC							1812
Db	181	TTGTCTGGCTTTTGGCACTCTCTGCCATTTCTGTGACGCTGACAGTGGCTCCCTGCCAGC							240
QY	1813	CTGCTCCTCCCTTAACCCCTTGTCGCCAAGGGGTGATGGCGGCTGGTTGTGGGCACTGGCG							1872
Db	241	CTGCTCCTCCCTTAACCCCTTGTCGCCAAGGGGTGATGGCGGCTGGTTGTGGGCACTGGCG							300
QY	1873	GTCAAGTGTGGAGAGAGAGGGGTGGAGGCTGCCCATTTAGATATCTTCCTGAGTCTTT							1932
Db	301	GTCAAGTGTGGAGAGAGAGGGGTGGAGGCTGCCCATTTAGATATCTTCCTGAGTCTTT							360
QY	1933	CCAGGGGCGCAATTTTGGATGAGCATGAGAGCTGTCACCTCAGCTCAGCTGTGGATGACTTGAG							1992
Db	361	CCAGGGGCGCAATTTTGGATGAGCATGAGAGCTGTCACCTCAGCTCAGCTGTGGATGACTTGAG							420
QY	1993	ATGAAAAAGAGAGACATGAGAAAGGGAACACAGCCAGGTGGACCTGACAGCGGCTG-CCTC							2051
Db	421	ATGAAAAAGAGAGACATGAGAAAGGGAACACAGCCAGGTGGACCTGACAGCGGCTG-CCTC							480
QY	2052	TGGGGCCACTTGTGATGTTCGCCACAGCTCCTCCACAAAGGAGTTTGTGATGGGTT							2111
Db	481	TGGGGCCACTTGTGATGTTCGCCACAGCTCCTCCACAAAGGAGTTTGTGATGGGTT							540
QY	2112	CTTAAGAGCTTAAGCAGCCCTGGATGGTGGCCAGAAATTAAGGAGACAGCCCTTCATGGGT							2171
Db	541	CTTAAGAGCTTAAGCAGCCCTGGATGGTGGCCAGAAATTAAGGAGACAGCCCTTCATGGGT							599
QY	2172	GGTGACGTGTGATGTCACCTTGTAAAGGGAACAGAA							2206
Db	600	GGGAGCAGGNGNAATCACTTGTAAAGGGAACANAAAA							634

RESULT 9

BM126575/c

LOCUS

BM126575

DEFINITION

1699a04.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

ACCESSION

CNA clone IMAGE:5675022 3', mRNA sequence.

VERSION

BM126575

KEYWORDS

BM126575.1 GI:17121127

SOURCE

human.

ORGANISM

homo sapiens

REFERENCE

1 (bases 1 to 553)

AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searles,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas 'M., Gibbons,M., McCann,R., Cole,R., Tsagarelisvilli,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE

Endocrine Pancreas Consortium

JOURNAL

Unpublished (2000)

COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmellone@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Juliana Brown
 (brownj@fas.harvard.edu) This sequence now available from the IMAGE
 consortium, for clone orders contact: info@image.llnl.gov
 Seq primer: -400P from GIBCO
 High quality sequence stop: 452.

FEATURES

source

1..553
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5675022"
 /clone_1id="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
 Site_2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT 175 a 121 c 114 g 143 t
 ORIGIN

Query Match 16.1%; Score 553; DB 13; Length 553;

Best Local Similarity 100.0%; Pred. No. 4.1e-117;

Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2663 TTGCAAAAATGACGTGGCTCCGACTTACGTTCTATTAATGAAAGTGTGAAGCAAAATG 2722
 DB 553 TTGCAAAAATGACGTGGCTCCGACTTACGTTCTATTAATGAAAGTGTGAAGCAAAATG 494
 OY 2723 CCCATGCTGGCGGCGAAGAGATGCTTTTGTGGAAGTCTCTGTGCTCCCTT 2782
 DB 493 CCCATGCTGGCGGCGAAGAGATGCTTTTGTGGAAGTCTCTGTGCTCCCTT 434
 OY 2783 CCATGCTGTGGGTTTCCAAAGGAGGAGGCTCCCTTTTGCAATGCCATTAAC 2842
 DB 433 CCAATGCTGTGGGTTTCCAAAGGAGGAGGCTCCCTTTTGCAATGCCATTAAC 374
 OY 2843 CATGAGCACTACTACCATGTTCTGCTGCGCAAGAGGCTGGTTTGCAAGAAATG 2902
 DB 373 CATGAGCACTACTACCATGTTCTGCTGCGCAAGAGGCTGGTTTGCAAGAAATG 314
 OY 2903 AAATGAATGATTTCTACAGCTTAACCTTGAAATGAAAGTCTTGCAATCCCATTT 2962
 DB 313 AAATGAATGATTTCTACAGCTTAACCTTGAAATGAAAGTCTTGCAATCCCATTT 254
 OY 2963 GCAGAGTCCGCTGTGCGACATGCTCTGTAGAGACACATCCAGGAGACTTGGAAC 3022
 DB 253 GCAGAGTCCGCTGTGCGACATGCTCTGTAGAGACACATCCAGGAGACTTGGAAC 194
 OY 3023 AGTTGGCACTTAAGAGTCTGCTCCCAAGACATCTTAAAGGTTTGAATGAGTGA 3082
 DB 193 AGTTGGCACTTAAGAGTCTGCTCCCAAGACATCTTAAAGGTTTGAATGAGTGA 134
 OY 3083 AAACGTTCTCTCTTATTTATGTTATGTAACAAGTGTGCTCTTTT 3142
 DB 133 AAACGTTCTCTCTTATTTATGTTATGTAACAAGTGTGCTCTTTT 74

OY 3143 GTATCTTTTAACTGTAAGTTCATGTAAGAAATGATATCATGCAATTAATATG 3202
 DB 73 GTATCTTTTAACTGTAAGTTCATGTAAGAAATGATATCATGCAATTAATATG 14
 OY 3203 CGATTTTCTTTC 3215
 DB 13 CGATTTTCTTTC 1

RESULT 10

BM126828

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 545)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lentshka,I., Scarsie,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,D., Blistain,A.,
 Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
 M., Gibbons,M., McCann,R., Cole,R., Tsagarashvilli,R., Williams,T.,
 Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other-ESTs: le99a04.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmellone@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Juliana Brown
 (brownj@fas.harvard.edu) This sequence now available from the IMAGE
 consortium, for clone orders contact: info@image.llnl.gov
 Seq primer: -400P from GIBCO
 High quality sequence stop: 430.

FEATURES

source

1..545
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5675022"
 /clone_1id="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
 Site_2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT

ORIGIN

143 a 113 c 121 g 168 t

[illegible]

	source	1. 591	/organism="Homo sapiens"	
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			/clone="S6SN620s1-19-D05"	
			/clone_1lb="S6SN620s1"	
			/sex="F"	
			/tissue_type="Ascites"	
			/cell_type="Scattering floating"	
			/cell_line="SNU-620"	
			/lab_host="Top10F"	
			/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;	
			Site_2: NotI; The poly (A)+ RNA was dephosphorylated with	
			bacterial alkaline phosphatase (BAP) and then decapped	
			with Tabacco acid pyrophosphatase (TAP). The decapped	
			intact mRNA was ligated with DNA-RNA linker including EcoR	
			I site by treatment of T4 RNA ligase and the first strand	
			cDNA was synthesized from oligo dt-selected mRNA by	
			priming with dt-tailed vector. The dt-tailed vector was	
			adjusted to have about 60nt. The cDNA vector was	
			clucularized with E. coli DNA ligase after digestion of	
			EcoRI which site is also included in vector. An RNA strand	
			converted to a DNA strand by Okayama-Berg method. The	
			obtained cDNA vectors were used for transformation of	
			competent cells E. coli Top10F by electroporation method.	
			The cDNA libraries constructed by this method are	
			full-length enriched cDNA library. After analyzing and	
			sequencing about 2,000 - 3,000 colonies in original cDNA	
			library, the abundant cDNAs were selected and amplified by	
			PCR reaction using vector region primer including T7	
			promotor as 5' primer and N(dt)14 as 3' primer. The PCR	
			products were used as template for synthesis of	
			biotinylated single stranded RNA by in vitro transcription	
			reaction. The synthesized RNA probes were hybridized with	
			antisense single stranded cDNAs prepared from original	
			library and incubated with avidin-gel. After removing	
			DNA-RNA hybrids by centrifuge, the subtracted cDNA	
			libraries were constructed by transformation of the	
			remaining DNA into competent cells E. coli Top10F with	
			electroporation method."	
BASE COUNT	128 a	149 c	169 g	145 t
ORIGIN				
Query Match	15.7%	Score 540.2;	DB 14;	Length 591;
Best Local Similarity	98.7%;	Pred. No. 3.8e-114;		
Matches 587;	Conservative 0;	Mismatches 3;	Indels 5;	Gaps 4;
OY 1999 AAGGAGACACTGGAAAGGAGACAGCCAGGTGCACCTCGACGGCGTC-CCTCTGGGCC 2057				
Db 1 AAGGAGAACAATGGAAAAGGAGACAGCCAGGTGCACCTCGACGGCGTCCTCTGGGCC 60				
OY 2058 CACTTGTAAGTGCACCAGCTACCTCTCCCAAGGGGAATTTCGTGATGGTTCTTGA 2117				
Db 61 CACTTGTAAGTGCACCAGCTACCTCTCCCAAGGGGAATTTCGTGATGGTTCTTGA 120				
OY 2118 GCCTTAGAGCCCTCGATGTGTGGCCAGAAAAAAGGAGCACACCCCTCATGGTGGTAGC 2177				
Db 121 GCCTTAGAGCCCTCGATGTGTGGCCAGAAAAAAGGAGCACACCCCTCATGGTGGTAGC 180				
OY 2178 GTGTAGTACCTCTGTAAAGGGAACAGAACTTTTGTCTTATGGGTAGAAATATAG 2237				
Db 181 GTGTAGTACCA-CTGTAAAGGGAACAGAACTTTTGTCTTATGGGTAGAAATATAG 239				
OY 2238 ACAATGCCCTTGGGTGGAGGGAAGCAATTGAAAAAGAACCTTGCCCTAGACATCCCTGGT 2297				
Db 240 ACAATGCCCTT-GGTGGAGGGAAGCAATTGAAAAAGAACCTTGCCCTAGACATCCCTGGT 298				
OY 2298 GCAGGTCTCCACCTGCACATTTGGGTGGGGCTCTGTGGAGGAGACTAGCCTTCTCTCC 2357				
Db 299 GCAGGTCTCCACCTGCACATTTGGGTGGGGCTCTGTGGAGGAGACTAGCCTTCTCTCC 358				
OY 2358 ATTCCTCCCTGCACCTGCTCTAGACACCTGGAGAGATGACATGCCCCCTTGCTCTGGCA 2417				
Db 359 ATTCCTCCCTGCACCTGCTCTAGACACCTGGAGAGATGACATGCCCCCTTGCTCTGG--C 416				

QY 2418 GGGGCGCAAGTCTGGACACATGTTGGCTCTTACAGGCTCTAGTCACTGGAATTGAG 2477
 DB 417 AGGGCGCAAGTCTGGACACATGTTGGCTCTTACAGGCTCTAGTCACTGGAATTGAG 476
 QY 2478 GTCCATGGGGGAATTCAGAGATGCTCACTTAAGGTACAGTCTTCCATGTTATCTTCT 2537
 DB 477 GTCCATGGGGGAATTCAGAGATGCTCACTTAAGGTACAGTCTTCCATGTTATCTTCT 536
 QY 2538 ACACATGCTACCTCAGTCTCTCTGGAACCTTACCTTTGATGTCGCAAGTACT 2592
 DB 537 ACACATGCTACCTCAGTCTCTCTGGAACCTTACCTTTGATGTCGCAAGTACT 591

RESULT 12 533 bp mRNA linear EST 06-MAR-2002
 BM829557
 LOCUS K-EST0102582 S9SNU601 Homo sapiens cDNA clone S9SNU601-59-G07 5',
 DEFINITION mRNA sequence.

ACCESSION BM829557
 VERSION BM829557.1 GI:19185966
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 533)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 59 row: G column: 07
 High quality sequence stop: 533.

FEATURES
 SOURCE Location/Qualifiers

1..533
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 /db_xref="taxon:9606"
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 /clone_1lb="S9SNU601"
 /sex="M"
 /tissue_type="Ascites"
 /cell_type="Epithelial"
 /lab_host="SNU-601"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pME18-FL3; site: 1: XhoI;
 site: 2: XhoI. The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including SfiI
 site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized with Superscript II using SfiI
 oligo-dT primer. After first strand synthesis, RNA was
 degraded by NaOH treatment and cDNA was amplified by PCR
 reaction. The PCR products were digested with SfiI and
 cloned into DraIII-digested pME185-FL3 vector. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

BASE COUNT 115 a 126 c 151 g 141 t
 ORIGIN

Query Match 15.5%; Score 533; DB 14; Length 533;
 Best Local Similarity 100.0%; Pred. NO. 1.7e-112;
 Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 GGTGCTTCATTTGAGACACAGAGATGCAACAGCAGATATGTATGACAACTGATCAC 1411
 DB 1 GGTGCTTCATTTGAGACACAGAGATGCAACAGCAGATATGTATGACAACTGATCAC 60
 QY 1412 ACCAGCATTGATCTGTGCGGCTTCTCTCAGAGGGAGTCTGATTTCTCCAGGGTGACAG 1471
 DB 61 ACCAGCATTGATCTGTGCGGCTTCTCTCAGAGGGAGTCTGATTTCTCCAGGGTGACAG 120
 QY 1472 TGGAGGGCTCTGGTGCACCTTGGCAAGCAATATGCTGGGCGATAGGGGATACAGCTG 1531
 DB 121 TGGAGGGCTCTGGTGCACCTTGGCAAGCAATATGCTGGGCGATAGGGGATACAGCTG 180
 QY 1532 GGGTTCGTGCTGTGCGCAAGCTTACAGACAGAGATGTACGGGATGTGATGATTTAC 1591
 DB 181 GGGTTCGTGCTGTGCGCAAGCTTACAGACAGAGATGTACGGGATGTGATGATTTAC 240
 QY 1592 GCACTGCAATTTATGACAAATGAGGGGACAGAGGCTAATTCACATGCTTGTGCTTGAC 1651
 DB 241 GCACTGCAATTTATGACAAATGAGGGGACAGAGGCTAATTCACATGCTTGTGCTTGAC 300
 QY 1652 GTCGTTTACAAAGAAACAAATGAGGGGCTGTTTGTCTCCGCTGATGATTTACTCTAG 1711
 DB 301 GTCGTTTACAAAGAAACAAATGAGGGGCTGTTTGTCTCCGCTGATGATTTACTCTAG 360
 QY 1712 AGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGAATGTGTGCTTGGCAGCTC 1771
 DB 361 AGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGAATGTGTGCTTGGCAGCTC 420
 QY 1772 TCTGCCATTCGTGTGACAGCTGACATGCTCCCTCCAGAGCTGTCTTCCCTAACCCCTT 1831
 DB 421 TCTGCCATTCGTGTGACAGCTGACATGCTCCCTCCAGAGCTGTCTTCCCTAACCCCTT 480
 QY 1832 GTCCCAAGGGGTGATGGCCGGCTGTTGTGGGCACTGGCGTCAAGTGTGA 1884
 DB 481 GTCCCAAGGGGTGATGGCCGGCTGTTGTGGGCACTGGCGTCAAGTGTGA 533

RESULT 13 529 bp mRNA linear EST 09-MAR-2000
 AM058537/c
 LOCUS W23D08.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544471 3',
 DEFINITION similar to SW:TW52_HUMAN O13933 TRANSMEMBRANE PROTEASE, SERINE 2 ;,
 mRNA sequence.

ACCESSION AM058537
 VERSION AM058537.1 GI:5934176
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 529)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/biop/image/image.html
 Insert length: 543 Std Error: 0.00
 Seq primer: -400P from Gldco
 High quality sequence stop: 319.

FEATURES
 SOURCE Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"

RESULT 15
AI826806/c 489 bp mRNA linear EST 07-MAR-2000
LOCUS w556e02.x1 NCI_CGAP_Pr22 Homo sapiens CDNA clone IMAGE:241948 3',
DEFINITION mRNA sequence.
ACCESSION AI826806 GI:5447477
VERSION AI826806.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 489)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Insert Length: 672 Std Error: 0.00
Seq primer: -400P from Glenco
High quality sequence stop: 480.
location/Qualifiers
1. 489
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:241948"
/clone_id="NCI_CGAP_Pr22"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/note="Organ: prostate; Vector: p773d-pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - o1190(dt) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p773 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 156 a 105 c 101 g 127 t
ORIGIN

Query Match 13.8% Score 475.4; DB 9; Length 489;
Best Local Similarity 99.6%; Pred. No. 3.6e-99;
Matches 487; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2735 GCGAAGAGAGAAAGATGTTTGTGACTCTGTGTCCTTCCAATGCTGTG 2794
|||||
DB 489 GCGAAGAGAGAAAGATGTTTGTGACTCTGTGTCCTTCCAATGCTGTG 430
|||||

OY 2795 GTTTCACACAGGAGGATCCCTTTTGCATGCGCAAGTCCATACCATGAGCATAC 2854
|||||
DB 429 GTTTCACACAGGAGGATCCCTTTTGCATGCGCAAGTCCATACCATGAGCATAC 370
|||||

OY 2855 TCTACCATGTTGCTGCTCCGCGGCAAGCAGGCTGTGCAAGAATGAATGAATGATT 2914
|||||
DB 369 TCTACCATGTTGCTGCTCCGCGGCAAGCAGGCTGTGCAAGAATGAATGAATGATT 310
|||||

OY 2915 CTACAGCTAGAGCTTAACCTTGAATGGAAGTCTTGCAATCCATTGCA -GGATCCGT 2973
|||||
DB 309 CTACAGCTAGAGCTTAACCTTGAATGGAAGTCTTGCAATCCATTGCAAGGATCCGT 250
|||||

OY 2974 CTGTGCACATGCTCTGTAGAGAGCAGATTCCAGGAGCCTTGAAACAGTGTGGCACTWG 3033
|||||

DB 249 CTGTGCACATGCTCTGTAGAGAGCAGCATTCCAGGAGCCTTGAAACAGTGTGGCACTG 190
|||||

OY 3034 TAAGTGTCTGTCCTCCCAAGACACATCCTAAAGGTTGTAAAGTGTAAGAAACGCTTCC 3093
|||||

DB 189 TAAGTGTCTGTCCTCCCAAGACACATCCTAAAGGTTGTAAAGTGTAAGAAACGCTTCC 130
|||||

OY 3094 TTCTTTATTTGCCCTTCTTATTTATGTGAACAACGTTTGTCTTTTGTATCTTTT 3153
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DB 129 TTCTTTATTTGCCCTTCTTATTTATGTGAACAACGTTTGTCTTTTGTATCTTTT 70
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OY 3154 AAACGTAAAGTTCATTTGTGAAAAATGAATATCATGCAATAATATATGCAATTTT 3213
|||||

DB 69 AAACGTAAAGTTCATTTGTGAAAAATGAATATCATGCAATAATATATGCAATTTT 10
|||||

OY 3214 TCAAGTAA 3222
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DB 9 TCAAGTAA 1
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Search completed: January 16, 2003, 08:12:59
Job time : 4228 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 18:24:31 ; Search time 1006 Seconds
(Without alignments)
1525.969 Million cell updates/sec

Title: US-09-807-201-8

Perfect score: 3443

Sequence: 1 gggcgggccggcgagtag.....ctgttcacatggcgtagata 3443

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3136.8	91.1	3245	9	US-10-012-896-929
2	3136.8	91.1	3245	9	US-09-895-793-929
3	3136.8	91.1	3245	9	US-09-895-814-929
4	3136.8	91.1	3245	10	US-09-759-143-929
5	3136.8	91.1	3245	10	US-09-780-669-929
6	3136.8	91.1	3245	10	US-09-822-827-929
7	2421	70.3	2486	9	US-09-981-353-22
8	2309.4	67.1	2479	9	US-10-012-896-894
9	2309.4	67.1	2479	9	US-09-895-793-894
10	2309.4	67.1	2479	9	US-09-895-814-894
11	2309.4	67.1	2479	10	US-09-759-143-894
12	2309.4	67.1	2479	10	US-09-780-669-894
13	2309.4	67.1	2479	10	US-09-822-827-894
14	1464.8	42.5	1479	9	US-10-012-896-930
15	1464.8	42.5	1479	9	US-09-895-793-930
16	1464.8	42.5	1479	9	US-09-895-814-930
17	1464.8	42.5	1479	10	US-09-759-143-930
18	1464.8	42.5	1479	10	US-09-780-669-930
19	1464.8	42.5	1479	10	US-09-822-827-930

20	1461.8	42.5	1476	9	US-10-012-896-931	Sequence 931, App
21	1461.8	42.5	1476	9	US-09-895-793-931	Sequence 931, App
22	1461.8	42.5	1476	9	US-09-895-814-931	Sequence 931, App
23	1461.8	42.5	1476	10	US-09-759-143-931	Sequence 931, App
24	1461.8	42.5	1476	10	US-09-780-669-931	Sequence 931, App
25	1461.8	42.5	1476	10	US-09-822-827-931	Sequence 931, App
26	983	28.6	1077	10	US-09-988-975A-2	Sequence 2, App1
27	681.4	19.8	683	9	US-10-012-896-896	Sequence 896, App
28	681.4	19.8	683	9	US-09-895-793-896	Sequence 896, App
29	681.4	19.8	683	9	US-09-895-814-896	Sequence 896, App
30	681.4	19.8	683	10	US-09-759-143-896	Sequence 896, App
31	681.4	19.8	683	10	US-09-780-669-896	Sequence 896, App
32	681.4	19.8	683	10	US-09-822-827-896	Sequence 896, App
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34	490	14.2	557	9	US-09-895-793-384	Sequence 384, App
35	490	14.2	557	9	US-09-895-814-384	Sequence 384, App
36	490	14.2	557	10	US-09-759-143-384	Sequence 384, App
37	490	14.2	557	10	US-09-780-669-384	Sequence 384, App
38	398.4	11.6	400	9	US-09-822-827-384	Sequence 384, App
39	398.4	11.6	400	9	US-09-232-880-325	Sequence 325, App
40	398.4	11.6	400	9	US-10-012-896-325	Sequence 325, App
41	398.4	11.6	400	9	US-09-895-793-325	Sequence 325, App
42	398.4	11.6	400	9	US-09-895-814-325	Sequence 325, App
43	398.4	11.6	400	10	US-09-759-143-325	Sequence 325, App
44	398.4	11.6	400	10	US-09-780-669-325	Sequence 325, App
45	398.4	11.6	400	10	US-09-822-827-325	Sequence 325, App

ALIGNMENTS

RESULT 1
US-10-012-896-929

Sequence 929, Application US/10012896
Publication No. US20020183251A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuguang
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick L.
APPLICANT: Wang, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanade, Yoshitiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 929
LENGTH: 3245
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-929

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Oy 2173 GTGACGTGGTACACCTTGTGAAGGGAACAGAAACATTTTGTCTTAATGGGGTGAGAA 2232
Db 2169 GTAGCTGGTACTCA-CCTGTAAGGGGAACAGAAACATTTTGTCTTAATGGGGTGAGAA 2227
Oy 2233 TATACACAGTGGCTTGGGTGGAGGGAACAAATGAAAAAGACTTGGCTGAGACATC 2292
Db 2228 TATACACAGTGGCTTGGGTGGAGGGAACAAATGAAAAAGACTTGGCTGAGACATC 2286
Oy 2293 CTTGGGAGGTGCTCCACCGACATTTGGGTGGGGCTCCGGAGGAGAGACTCAGCCCTTGC 2352
Db 2287 CTGGTGAAGGTCTCCACCGACATTTGGGTGGGGCTCCGGAGGAGAGACTCAGCCCTTGC 2346
Oy 2353 TCCCTATCCCTCCCTGACCCCTGCTCCAGACCCCTGAGAGTGCACATGCCCCCTGGTCT 2412
Db 2347 TCCCTATCCCTCCCTGACCCCTGCTCCAGACCCCTGAGAGTGCACATGCCCCCTGGTCT 2406
Oy 2413 GGGGAGGGGGCCCAAGTCTGGGACCAATGTTGGCTCTTCAGGCTGCTAGTCACTGGAAA 2472
Db 2407 GG--CAGGGCCGCAAGTCTGGGACCAATGTTGGCTCTTCAGGCTGCTAGTCACTGGAAA 2464
Oy 2473 TTGAGGTCCATGGGGGAATCAAGATGCTCAGTTTAAGTACACGTTCATGTTATG 2532
Db 2465 TTGAGGTCCATGGGGGAATCAAGATGCTCAGTTTAAGTACACGTTCATGTTATG 2524
Oy 2533 TTTTACACATTTGCTACCTGCTGCTCCAGAACTTACCTTGTGATGCTCCAACTAGT 2592
Db 2525 TTTTACACATTTGCTACCTGCTGCTCCAGAACTTACCTTGTGATGCTCCAACTAGT 2584
Oy 2593 CCACCTTCACTTAACTCTTTGAACTGTATCATCTTTGCCAAGTAAGAGTGGGCTTAT 2652
Db 2585 CCACCTTCACTTAACTCTTTGAACTGTATCATCTTTGCCAAGTAAGAGTGGGCTTAT 2644
Oy 2653 TTTACGCTGTTTGAACAAATGATGGGCTCCCTACCTTAAGTCTTAATTAATGATGGC 2712
Db 2645 TTTACGCTGTTTGAACAAATGATGGGCTCCCTACCTTAAGTCTTAATTAATGATGGC 2704
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Db 2765 GTGGTCCCTTCCAAATGCTGTGGGTTTCCACCAAGGGAAGGTTCCCTTTGCACTTCCAA 2824
Oy 2833 GTGGCATAACATGAGCACTACTCTACATGCTGCTGCTGGCGCAAGGCTGGTT 2892
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RESULT 2
US-09-895-793-929
; Sequence 929, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocke, Susan L.
; APPLICANT: Jiang, YUQIU
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 929
; LENGTH: 3245
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-929

Query Match 91.1%; Score 3136.8; DB 9; Length 3245;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3197; Conservative 0; Mismatches 7; Indels 6; Gaps 5;

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Oy 74 GCGGCTGGAGCGGCGAGGCTATTTGAACATTTCCAGATACCTTATCATCTGATGCT 133
Db 70 GCGGCTGGAGCGGCGAGGCTATTTGAACATTTCCAGATACCTTATCATCTGATGCT 129
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Oy 194 GAACACATGATTAACCAACCGGAAACCCCTATTCGCCGACAGCCCACTGTGCTCCACT 253
Db 190 GAACACATGATTAACCAACCGGAAACCCCTATTCGCCGACAGCCCACTGTGCTCCACT 249
Oy 254 GTTACAGAGTGCATCGGCTCAGTACTACCTCCCGCTGGCCGAGTACGCGCCGAGG 313
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Oy 314 GTCTGACGAGGCTTCCAAACCCGCTGCTGTGCACGACGACCCAAATCCCATCCGAGACA 373
Db 310 GTCTGACGAGGCTTCCAAACCCGCTGCTGTGCACGACGACCCAAATCCCATCCGAGACA 369
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Db	490	TCTGGGATAGAGTGCAGATCTCTCAGATACCTGCATCAAAACCTCTAACTGGTGTATGGC	549
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QY	734	TCTAGCCAGGAATAGTGGATGACAGCGGATCCACAGCTTTATGAACGTGAACACAACT	793
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QY	914	ATCGTGGCGCGGAGAGCGGCTCCGGGGGCTGGCCCTGGGACAGTCAGCTGCACGT	973
Db	910	ATTGTGGCGCGCGAGAGCGGCTCCCGGGGGCTGGCCCT - GGCAAGTCAGCTGCACAGT	968
QY	974	CCAGAAAGCTCCACGATGAGCGGAGGCTCCATCATCACCCGAGTGGATGTGTGCAAGCGCG	1033
Db	969	CCAGAAAGCTCCACGATGAGCGGAGGCTCCATCATCACCCGAGTGGATGTGTGCAAGCGCG	1022
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QY	1094	GAGACAATCTTCAATGTTCTATGAGAGCCGATATCAAGTATGAAAAAGTATTTCTCATCC	1155
Db	1089	GAGACAATCTTCAATGTTCTATGAGAGCCGATATCAAGTATGAAAAAGTATTTCTCATCC	1148
QY	1154	AAATATATACCTCAAGACAAAGAAATATGATTTGGGCTATGATACCTGCAGAAAGCTCT	1211
Db	1149	AAATATATACCTCAAGACAAAGAAATATGATTTGGGCTATGATACCTGCAGAAAGCTCT	1206
QY	1214	GACTTTCAAGACCTAGTGAAAACCAAGTGTGTCTGCCCAACCCAGGCATGATGCTGCAGCC	1273
Db	1209	GACTTTCAAGACCTAGTGAAAACCAAGTGTGTCTGCCCAACCCAGGCATGATGCTGCAGCC	1268
QY	1274	AGAAAGCTGTGCTGATTTCCGGGTGGGGGCCACCGAGAGAGAAAGGGAAGACTCAGA	1333
Db	1269	AGAAAGCTGTGCTGATTTCCGGGTGGGGGCCACCGAGAGAGAAAGGGAAGACTCAGA	1328
QY	1334	AGTGTGAAGCTGCAGAAAGGTCTTCAATTGAGACACAGATGTGCACAGCAGATATGT	1393
Db	1329	AGTGTGAAGCTGCAGAAAGGTCTTCAATTGAGACACAGATGTGCACAGCAGATATGT	1388
QY	1394	CTATGACAACTGATTCACACACAGCCATGATCTGTCCGGGCTTCTCTCAGGGAGAGCTGCA	1453
Db	1389	CTATGACAACTGATTCACACACAGCCATGATCTGTCCGGGCTTCTCTCAGGGAGAGCTGCA	1448
QY	1454	TTTCTTGGCAGGGGTACAGATGAGAGGGCTCTGTGCTACTTTGGAAGACAAATCTGGTGGCT	1513
Db	1449	TTTCTTGGCAGGGGTACAGATGAGAGGGCTCTGTGCTACTTTGGAAGACAAATCTGGTGGCT	1508

QY	1514	GANAGGGATATCAAGCGGGGGTTCTGGCTGTGGCAAAAGCTTACACACAGAGGTACAG	1573
Db	1509	GATTAAGGGATATCAAGCGGGGGTTCTGGCTGTGGCAAAAGCTTACACACAGAGGTACAG	1568
QY	1574	GAATGTGATGTATTCACAGCAGCATGTATTTATCACAAATAGAGGGACAGAGCGTAAATCC	1633
Db	1569	GAATGTGATGTATTCACAGCAGCATGTATTTATCACAAATAGAGGGACAGAGCGTAAATCC	1628
QY	1634	ATGGTCCTGCTGCTTGGACGTCGTTTTACAAAGAAACAAATGGGGCTGTTTTGCTTCCCG	1693
Db	1629	ATGGTCCTGCTGCTTGGACGTCGTTTTACAAAGAAACAAATGGGGCTGTTTTGCTTCCCG	1688
QY	1694	TGCATGATTACTCTGTAGAGATGATTCAGAGGTCACCTTATTTTTATTAACATGAAAT	1733
Db	1689	TGCATGATTACTCTGTAGAGATGATTCAGAGGTCACCTTATTTTTATTAACATGAAAT	1748
QY	1754	TGTCGGCTTTGGACGTCCTGGCAATTCGTGACGCTGACAGGCTGCCCGCCACAC	1813
Db	1749	TGTCGGCTTTGGACGTCCTGGCAATTCGTGACGCTGACAGGCTGCCCGCCACAC	1808
QY	1814	TGCTCTCCCTAACCCCTTGTGTCGCAAGGGGTGATGCGCCGGCTGTGTGTGGACATGGGG	1873
Db	1809	TGCTCTCCCTAACCCCTTGTGTCGCAAGGGGTGATGCGCCGGCTGTGTGTGGACATGGGG	1868
QY	1874	TCAACTGTGAGAGAGAGGGGTGAGAGCTGCCCATTTAGATCTCTCTGCTAGTCTTTC	1933
Db	1869	TCAACTGTGAGAGAGAGGGGTGAGAGCTGCCCATTTAGATCTCTCTGCTAGTCTTTC	1928
QY	1934	CAGGGGCCAATTTTGGATGAGACATGAGAGCTGACCTGACCTGCTGATACATTTGAGA	1993
Db	1929	CAGGGGCCAATTTTGGATGAGACATGAGAGCTGACCTGACCTGCTGATACATTTGAGA	1988
QY	1994	TGAAAAAGAGAGACATGAGAAAGGAGACAGCAGGTGACCTGACAGGGCTG - CACT	2052
Db	1989	TGAAAAAGAGAGACATGAGAAAGGAGACACCAAGTGGACCTGAGAGGGCTGCTCT	2048
QY	2053	GGGGCCACTGTGTAGTGTCCCCACGCTACTCTTCACAAAGGGATTTGCTGATGGTTTC	2112
Db	2049	GGGGCCACTGTGTAGTGTCCCCACGCTACTCTTCACAAAGGGATTTGCTGATGGTTTC	2108
QY	2113	TTAGAGCCTTGGACGCCCTGGATGTGTGGCCAGAAATTAAGGGACACAGCCCTTCAATGGTG	2172
Db	2109	TTAGAGCCTTGGACGCCCTGGATGTGTGGCCAGAAATTAAGGGACACAGCCCTTCAATGGTG	2168
QY	2173	GTGAGCTGTGTAGTACCTTGTAAAGGGAAACAGAAATTTTGTGTTATGAGGGTGAATA	2232
Db	2169	GTGAGCTGTGTAGTACCTTGTAAAGGGAAACAGAAATTTTGTGTTATGAGGGTGAATA	2227
QY	2233	TATAGACAGTGCCTTGGGTGCGAGGGAAACATTTGAAAGAAAGAACTTGCCCTGAGCACTC	2292
Db	2228	TATAGACAGTGCCTT - GGTGCGAGGGAAACATTTGAAAGAAAGAACTTGCCCTGAGCACTC	2286
QY	2293	CTGGGTGACAGTCTCCACTGACATTTGGGTGGGGCTCTGGGAGGAGACTAGCCTTTC	2352
Db	2287	CTGGGTGACAGTCTCCACTGACATTTGGGTGGGGCTCTGGGAGGAGACTAGCCTTTC	2346
QY	2353	TGCTCATCTCCCTGACCTGCTGCTGACACCTTGAGAGTGCACATGCGCCCTTGCTGCT	2412
Db	2347	TGCTCATCTCCCTGACCTGCTGCTGACACCTTGAGAGTGCACATGCGCCCTTGCTGCT	2406
QY	2413	GGGCGAGGGCCCAAGTCTGGACACATTTGGGCTTTAGAGCCTGCTAGTACATGAGAA	2472
Db	2407	GG - CAGGGCCCAAGTCTGGACACATTTGGGCTTTAGAGCCTGCTAGTACATGAGAA	2464
QY	2473	TTGAGGTCCATGGGGAAATCAAGAGATGCTCAATTTAAGGTACACTGTTTCCATGTTATG	2532
Db	2469	TTGAGGTCCATGGGGAAATCAAGAGATGCTCAATTTAAGGTACACTGTTTCCATGTTATG	2534
QY	2533	TTTTCTACACATTTGCTACTGACAGTGTCTCTGAGAAACTTACTTTTATGTCTCACAATGAT	2592
Db	2525	TTTTCTACACATTTGCTACTGACAGTGTCTCTGAGAAACTTACTTTTATGTCTCACAATGAT	2584
QY	2593	CCACCTTATTTAATCTTTTGAACATGATACATTTGCAAGTAAAGTGTGGCAT	2652

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Oy 2653 TTACAGCTGCTTGAACAAATGAGTGGCTTCACTTAACTCTTAAATGATGCG 2712
Db 2645 TTACAGCTGCTTGAACAAATGAGTGGCTTCACTTAACTCTTAAATGATGCG 2704
Oy 2713 AAGCAAGTGGCCATGAGTGGCGGCAAGAAAGATGTTTGTGTTGGACTCT 2772
Db 2705 AAGCAAGTGGCCATGAGTGGCGGCAAGAAAGATGTTTGTGTTGGACTCT 2764
Oy 2773 GTGGTCCCTTCCAAATGCTGTGGGTTCCACAGGGAAGGTTCCCTTTGCAATG 2832
Db 2765 GTGGTCCCTTCCAAATGCTGTGGGTTCCACAGGGAAGGTTCCCTTTGCAATG 2824
Oy 2833 GTGGCATTAACCTAGAGTGGCTTCACTTACCTGCTTCCGCGCAAGAGCTG 2892
Db 2825 GTGGCATTAACCTAGAGTGGCTTCACTTACCTGCTTCCGCGCAAGAGCTG 2884
Oy 2893 TGCAGAAATGAATGAATGATCTACAGCTAGAGCTTAACTTGAATGAAAGTCT 2952
Db 2885 TGCAGAAATGAATGAATGATCTACAGCTAGAGCTTAACTTGAATGAAAGTCT 2944
Oy 2953 AATCCCATTTGAGAGATCCGTGTGACATGCTCTGTAGAGAGAGATCCCAAG 3012
Db 2945 AATCCCATTTGAGAGATCCGTGTGACATGCTCTGTAGAGAGAGATCCCAAG 3004
Oy 3013 CTTTGAAGAACTGAGTGGCTTGAAGTGGCTTGAAGTGGCTTGAAGTGGCT 3072
Db 3005 CTTTGAAGAACTGAGTGGCTTGAAGTGGCTTGAAGTGGCTTGAAGTGGCT 3064
Oy 3073 GTATGGAAGAACTGAGTGGCTTGAAGTGGCTTGAAGTGGCTTGAAGTGGCT 3132
Db 3065 GTATGGAAGAACTGAGTGGCTTGAAGTGGCTTGAAGTGGCTTGAAGTGGCT 3124
Oy 3133 GTCTTTTGTATCTTTTAACTGTAATGTAATGTAATGTAATGTAATGTAAT 3192
Db 3125 GTCTTTTGTATCTTTTAACTGTAATGTAATGTAATGTAATGTAATGTAAT 3184
Oy 3193 ATAAATTAAGCATTTTTCATCAAGTAA 3222
Db 3185 ATAAATTAAGCATTTTTCATCAAGTAA 3214

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RESULT 3

US-09-895-814-929

Sequence 929, Application US/09895814

Publication No. US20020193296A1

GENERAL INFORMATION:

APPLICANT: Xu, Jianshun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yugu
 APPLICANT: Kalos, Michael D.
 APPLICANT: Reiter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Derrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aljun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William T.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals de Bassols, Carlota
 APPLICANT: Foy, Teresa
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C26
 CURRENT APPLICATION NUMBER: US/09/895,814
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 990
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 929
 LENGTH: 3245
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-895-814-929

Query Match 91.1%; Score 3136.8; DB 9; Length 3245;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 3197; Conservative 0; Mismatches 7; Indels 6; Gaps 5;

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Db 10 CGGCTCGGCGAGCTAACAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 69
Oy 74 GCGGCTGGAGGCGGCGAGGCTATTTGAACATTTCCAGATTTACTATCTGATGCT 133
Db 70 GCGGCTGGAGGCGGCGAGGCTATTTGAACATTTCCAGATTTACTATCTGATGCT 129
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Oy 254 GTCTAGAGAGTGCATCCGCTCAGTACTACCCGCTCCGCGCGGCGGAGGCGGAGG 313
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Oy 494 TCTGGATAGAGTGCAGTCTCAGTACTGATCAACCCCTCTAATGTTGATGAGC 553
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Oy 554 GTGTGACCTGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 613
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Oy 854 GTGGTTCTTTAGCTGTATAGCTGCGGAGGAGTCACTGAATCAAGCCGAGAGCAGG 913

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Db 1869 TCAAGTGTGAGAGAGGGGCTGGAGGCTGCCCATTTGAGATCTTCTCTGAGTCTTTC 1928
Qy 1934 CAGGGGCAATTTTGGATGAGATGAGAGCTGACCTCTCAGCTGCTGATGACTTGA 1993
Db 1929 CAGGGGCAATTTTGGATGAGATGAGAGCTGACCTCTCAGCTGCTGATGACTTGA 1988

Qy 1994 TGAAGAGAGAGACATGGAAGAGAGACACAGGTGGCACTGTACAGCGGCTG -CCTCT 2052
Db 1989 TGAAGAGAGAGACATGGAAGAGAGACACAGGTGGCACTGTACAGCGGCTG -CCTCT 2048
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Db 2049 GGGGCACTTGTGTAGTGTCCCGAGCTACTCTCCACAGGGGATTTTGTGTATGGTTTC 2108
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Db 2347 TCTCATCTCCCTGACCCCTGCTCTAGCACCCCTGAGAGTGCACATGCCCTTGGTCT 2406
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Db 2407 GG -CAGGGCGCAAGTGTGCGACCATGTGGGCTCTTCAAGGCTGCTAGTCACTGCAAA 2464
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Db 2465 TTGAGTCCATGGGGGGAATCAAGGATGCTGAGTTTAAGTACACTGTTTCATGTTATG 2524
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Db 2585 CCACCTTATTTAACTCTTTGAACGTATCATCTTTGCCAAGTGAAGTGTGGCTAT 2644
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Db 2645 TTACGCTGCTTGAACAAATGACTGGCTCTGACTTAACTTAAATGAATGTGCTG 2704
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Db 2705 AAGCAAGTGGCCATGTTGGGCGGCAAGAGAAAGATGTGTTTGTGTTGGACTCT 2764
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Db 3005 CTTTGAAGAAAGTTGGCACTGTAAAGGTGCTGTCCCAAGACACATCTTAAAGGTGT 3064

Qy	3073	GTATGGTGAAGAAAGCTCTCCCTCTTATTTGGCCCCCTCTTATTTATGTGAACAATGTT	3132
Db	3065	GTAATGGTGAAGAAAGCTCTCCCTCTTATTTATGGCCCTCTTATTTATGTGAACAATGTT	3124
Qy	3133	GTCCTTTTGTGATCCTTTTAAAGCTGAAGTCAATGTGAANAATGAATTCATGCA	3192
Db	3125	GTCCTTTTGTGATCCTTTTAAACGTAAGTCAATGTGAANAATGAATTCATGCA	3184
Qy	3193	ATAAATTATGCGATTTTTTTTCAAGTAA	3222
Db	3185	ATAAATTATGCGATTTTTTTTCAAGTAA	3214

RESULT 4
US-09-759-143-929
; Sequence 929, Application US/09759143
; Patent No. US20020022248A1

```

1  APPLICANT:  Xu, Jiangchun
2  APPLICANT:  Dillon, Davin C.
3  APPLICANT:  Mitcham, Jennifer L.
4  APPLICANT:  Harlocker, Susan L.
5  APPLICANT:  Jiang, Yugu
6  APPLICANT:  Henderson, Robert A.
7  APPLICANT:  Kalos, Michael D.
8  APPLICANT:  Fanger, Gary R.
9  APPLICANT:  Reltter, Marc W.
10 APPLICANT:  Stolk, John A.
11 APPLICANT:  Day, Craig H.
12 APPLICANT:  Vedvick, Thomas S.
13 APPLICANT:  Carter, Darrick
14 APPLICANT:  Li, Samuel
15 APPLICANT:  Wang, Aljun
16 APPLICANT:  Skelky, Yasir A.W.
17 APPLICANT:  Hepler, William
18 TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
19 TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
20 FILE REFERENCE:  210121.427023
21 CURRENT APPLICATION NUMBER:  US/09/7759,143
22 NUMBER OF SEQ ID NOS:  934
23 SOFTWARE:  FastSeq for Windows Version 3.0
24 SEQ ID NO 929
25 LENGTH: 3245
26 TYPE: DNA
27 ORGANISM: Homo sapiens
28 US-09-759-143-929

```

Query Match	91.1%;	Score 3136.8;	DB 10;	Length 3245;
Best Local Similarly	99.68;	Pred. No. 0;		
Matches 1197; Conservative	0;	Mismatches	7;	Gaps 5;

QY	14	CGAGTATGGCCGGAGCTTAAGCAGGAGGGGAGGGGAGGGGAGGGGAGGGGAGG	73
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QY	74	GCCGCGCTGGAGCGCGGCGAGGTCATATTGAACATTCGAGATACCTATCTACTCGATGCT	133
Db	70	GCCCGCTGGAGCGCGGCGAGGTCATATTGAACATTCGAGATACCTATCTACTCGATGCT	129
QY	134	GTTGATTAACACCAAGATGGCTTTAACTCACTCAGGCGACACACCTATGTGACCTTACTAT	193
Db	130	GTTGATTAACACCAAGATGGCTTTAACTCACTCAGGCGACACACCTATGTGACCTTACTAT	189
QY	194	GAATAACCATGATATCAACAACGGAAAAACCCCTATTCGCCACAGGCCATCTGTGCTCCACT	253
Db	190	GAATAACCATGATATCAACAACGGAAAAACCCCTATTCGCCACAGGCCATCTGTGCTCCACT	249
QY	254	GTCATACGAGGTGTCATCCGGGCTCATACTACCCGTCGCCCGCTGCCCGCAGTACGCCCGGAGG	313
Db	250	GTCATACGAGGTGTCATCCGGGCTCATACTACCCGTCGCCCGCTGCCCGCAGTACGCCCGGAGG	309
QY	314	GTCCTGACAGCGGCTTCCAAACCCCGTGTCTGCACGCGAGGCCAAATCCCATCCGGGACA	373

Db	310	GTCCGAGGAGGGTTCCAAACCCCGTGTGTGACGACCAACCAATTCOCATCCGGGACA	369
QY	374	GTGTGCACCTCCAAAGACTAAAGAAAGCACTGTGCATCTACCTTAACCTTGGGACCTTCTC	433
Db	370	GTGTGCACCTCCAAAGACTAAAGAAAGCACTGTGCATCTACCTTAACCTTGGGACCTTCTC	429
QY	434	GTGGGAGCTGGCGTGGCGGTGGCGTCACTGTGCAATTTATGAGGAGCAAGCGTCCAC	493
Db	430	GTGGGAGCTGGCGTGGCGGTGGCGTCACTGTGCAATTTATGAGGAGCAAGCGTCCAC	489
QY	494	TCCTGGATAGAGTGCAGCTCCTCAGGTACCTGCATCAACCCCTTAACTGTGTGATGGC	553
Db	490	TCCTGGATAGAGTGCAGCTCCTCAGGTACCTGCATCAACCCCTTAACTGTGTGATGGC	549
QY	554	GTGTCACTATGCCCCGGGGGGGAGAGAGAAATCGGTGTGTTCGGCTCTAGGGACCAAC	613
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QY	614	TTTCATCCCTTCAGGTACTCATCTCAAGAGAAATCTGACACCTGTGCGCAACAGAC	673
Db	610	TTTCATCCCTTCAGGTACTCATCTCAAGAGAAATCTGACACCTGTGCGCAACAGAC	669
QY	674	TGGAAACGAACTACGCGCGCGCGCCCTCGAGGACATGGCTATPAAGATATTTTATC	733
Db	670	TGGAAACGAACTACGCGCGCGCGCCCTCGAGGACATGGCTATPAAGATATTTTATC	729
QY	734	TCCTAGCCAAAGAAATAGAGGATGACGAGGATCCACAGCTTATGAACCTGAACCAAGT	793
Db	730	TCCTAGCCAAAGAAATAGAGGATGACGAGGATCCACAGCTTATGAACCTGAACCAAGT	789
QY	794	GCCGGCAATGTGATATCTATAAAAAACTGTACACAGTATGCTGTCTTCAAAACGA	853
Db	790	GCCGGCAATGTGATATCTATAAAAAACTGTACACAGTATGCTGTCTTCAAAACGA	849
QY	854	GTGTTTCTTTACCTCTTATAGCTCGGGGGGTCAATTGAATCAAGCGCCGACAGCAGG	913
Db	850	GTGTTTCTTTACCTCTTATAGCTCGGGGGGTCAATTGAATCAAGCGCCGACAGCAGG	909
QY	914	ATCGTGGCGCGCGAGACCGCGCTCCCGGGGGCTCGCCCTGGGGAGGTAGCTCCACGT	973
Db	910	ATCGTGGCGCGCGAGACCGCGCTCCCGGGGGCTCGCCCTGGGGAGGTAGCTCCACGT	968
QY	974	CCAGACGCTCCACGTGTGCGGAGGCTCATCATACCCCCGAGTGGATCTGACAGCCGC	1033
Db	969	CCAGACGCTCCACGTGTGCGGAGGCTCATCATACCCCCGAGTGGATCTGACAGCCGC	1028
QY	1034	CCAGCGGTGGAAAAACCTCTTAAACAATCCATGGCAATGGAGGCAATTTGGCGGGATTTT	1093
Db	1029	CCAGCGGTGGAAAAACCTCTTAAACAATCCATGGCAATGGAGGCAATTTGGCGGGATTTT	1088
QY	1094	GAGACATCTTTCATGTGTCTATGAGCGCGATACCAAGTAGAAAAAGTATTTTCATCC	1153
Db	1089	GAGACATCTTTCATGTGTCTATGAGCGCGATACCAAGTAGAAAAAGTATTTTCATCC	1148
QY	1154	AAATTAATGACTCCAAAGACCAAGAACAATGACATTTGGCGTGAATGAACTCGAGACCTCT	1213
Db	1149	AAATTAATGACTCCAAAGACCAAGAACAATGACATTTGGCGTGAATGAACTCGAGACCTCT	1208
QY	1214	GACTTTCAACACCTAGTGAAGACAGTGTCTGCCCCAACCCAGGATATCTCTGACGC	1273
Db	1209	GACTTTCAACACCTAGTGAAGACAGTGTCTGCCCCAACCCAGGATATCTCTGACGC	1268
QY	1274	AGAACACGCTGTGTGATTTTCCGGGTGGGGGCGCACCGAGAGAAAAGGAGAACCTCAGA	1333
Db	1269	AGAACACGCTGTGTGATTTTCCGGGTGGGGGCGCACCGAGAGAAAAGGAGAACCTCAGA	1328
QY	1334	AGTGTGAAGCTTCGCAAGGAGCTTCATTTGAGACACAGAAATGCAACAGCAGATATGT	1393
Db	1329	AGTGTGAAGCTTCGCAAGGAGCTTCATTTGAGACACAGAGTGAACAGCAGATATGT	1388
QY	1394	CTATGCAACACTGTATCAACACAGCAATGATCTGTCCGGCTTCTGCAAGGGAGAGTTCGA	1453

Db	1389	CTATGACACCGTATATACACACACACCGCATGATCTGTGCGGCTTCTGCGAGGGAAAGCTGCA	1448
Qy	1454	TTCTTCCGCAAGGCTGACAGTGGAGAGGGCCCTGTGCTCACTTCGGAAGAACATATCTGTGGCT	1513
Db	1449	TTCTTCCGCAAGGCTGACAGTGGAGAGGGCCCTGTGCTCACTTCGGAAGAACATATCTGTGGCT	1508
Qy	1514	GATAGGGGATATCAAGCGGGGTTCTGGCTGTGCGCAAGGCTTCACAGCCAGAGAGTGTACGG	1573
Db	1509	GATAGGGGATATCAAGCGGGGTTCTGGCTGTGCGCAAGGCTTCACAGCCAGAGAGTGTACGG	1568
Qy	1574	GAATGTGATGGTATATCACGGACCTGATTTATCGACAAATGAGGGGACAGCGGCTAATCCAC	1633
Db	1569	GAATGTGATGGTATATCACGGACCTGATTTATCGACAAATGAGGGGACAGCGGCTAATCCAC	1628
Qy	1634	ATGGTCTTCTGCTCTTGACAGCTGTTTACAAAGAAACATGGGGCTGTGTTTGTCTCCCG	1693
Db	1629	ATGGTCTTCTGCTCTTGACAGCTGTTTACAAAGAAACATGGGGCTGTGTTTGTCTCCCG	1688
Qy	1694	TGCATGATTTACTCTTAGAAGATGATTCAGAGGTCACCTTATTTATTAACAGTGAAC	1753
Db	1689	TGCATGATTTACTCTTAGAAGATGATTCAGAGGTCACCTTATTTATTAACAGTGAAC	1748
Qy	1754	TGTCGTGCTTTGGACACTCTTGCCACTTCTGTGCGAGGCTGCACTGGCTCCCTGCGCCAGC	1813
Db	1749	TGTCGTGCTTTGGACACTCTTGCCACTTCTGTGCGAGGCTGCACTGGCTCCCTGCGCCAGC	1808
Qy	1814	TGCTCTCTCCCTAACCCCTTGTCTGCGCAAGGGGTAGTGCGCGCTGTGTGGGACACTGCGG	1873
Db	1809	TGCTCTCTCCCTAACCCCTTGTCTGCGCAAGGGGTAGTGCGCGCTGTGTGGGACACTGCGG	1868
Qy	1874	TCAAGTGTGGGGAGAGGGGTGGAGGCTGCCCATTTGAGATCTTCCTGCTGACAGTCTTTC	1933
Db	1869	TCAAGTGTGGGGAGAGGGGTGGAGGCTGCCCATTTGAGATCTTCCTGCTGACAGTCTTTC	1928
Qy	1934	CAGGGGCCAATTTTGGATGAGCATGAGCGTGTACCTCTCAGCTGCTGATGAGACTTGAGA	1993
Db	1929	CAGGGGCCAATTTTGGATGAGCATGAGCGTGTACCTCTCAGCTGCTGATGAGACTTGAGA	1988
Qy	1994	TGAAAAAGAGAGACATGGAAGGGAGACGCCAGGTGGCACCTGCGAGCGGCTG - CCTCT	2052
Db	1989	TGAAAAAGAGAGACATGGAAGGGAGACGCCAGGTGGCACCTGCGAGCGGCTGCGCCCT	2048
Qy	2053	GGGGCCACTTGGTAGTGTGCCCGAGCCTACCTCCACAAAGGGGATTTGTGCGTAGTGGGTC	2112
Db	2049	GGGGCCACTTGGTAGTGTGCCCGAGCCTACCTCCACAAAGGGGATTTGTGCGTAGTGGGTC	2108
Qy	2113	TTAGAGCCTTAGAGAGCCCTGGATGTGTGGCCAGAAATTAAGGAGCAGCGCTTACATGGGTG	2172
Db	2109	TTAGAGCCTTAGAGAGCCCTGGATGTGTGGCCAGAAATTAAGGAGCAGCGCTTACATGGGTG	2168
Qy	2173	GTACAGCTGTAGTACACTTGTGAAGGGGAAACAGAAACATTTTGTCTTATGGGTGAGAA	2232
Db	2169	GTACAGCTGTAGTACACTTGTGTGAAGGGGAAACAGAAACATTTTGTCTTATGGGTGAGAA	2227
Qy	2233	TATAGACAGTGGCCTTGTGGTGGCAGAGGGAAGCAATTGAAAAGGAACCTGTGCTGAGCACTC	2292
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Qy	2293	CTGTGTGACAGCTGTACACTTCACATTTGGGTGGGGGCTCCGGGAGGGAGATCAGACCTTTC	2352
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Qy	2353	TCTCATCTCTCCCTGAGCCCTGTCTTAGACACCTGTGAGAGTGCACATGCCCCCTGTGTCT	2412
Db	2347	TCTCATCTCTCCCTGAGCCCTGTCTTAGACACCTGTGAGAGTGCACATGCCCCCTGTGTCT	2406
Qy	2413	GGGCGAGGGGGCCCAAGTCTTGCGACCACTGTTGGCTCTTGAGGCTGTCTAGTCACTGGAAA	2472
Db	2407	GG - CAGGGGGCCCAAGTCTTGCGACCACTGTTGGCTCTTGAGGCTGTCTAGTCACTGGAAA	2464
Qy	2473	TTTGAGGTCCATGGGGGAAATCAAGGATGTGCGATTTAAGGTGCACATGTTTCCATGTTATG	2532
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RESULT 5
US-09-780-669-929
; Sequence 929, Application US/09780669
; Patent No. US20020051977A1

GENERAL INFORMATION

APPLICANT: Xu, Jia

APPLICANT: Dillion,

APPLICANT: Mitchar

APPLICANT: Harjot

APPLICANT: Tiana

ADDRESS: 11000

APPLICANT: Henders

APPLICANT: KALOS,

APPLICANT: Fanger,

APPLICANT: Retter,

APPLICANT: Stolk,

	DAY	CITY	APPLICANT:
1			
2			
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ADDITIONAL: Vedvici

ADDITONAL: 02-40

APPLICANT: Carter,

APPLICANT: J.J. San

APPLICANT: Wang, Z

APPLICANT: Skeiky

APPLICANT: Herley

APPLICANT: Rural

/ s m y n u : t a l l e c t e d i


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|||||
Db 490 TCTGGATAGATGAGCTCTCAGATCAACCCCTCACTGCTATGAC 549
QY 554 GTGTACACTGCCCCGGGGGAGAGAGATCGGTGTGTCGCTCAGGACCAAC 613
Db 550 GTGTACACTGCCCCGGGGGAGAGAGATCGGTGTGTCGCTCAGGACCAAC 609
QY 614 TTCACTCTTCAAGTGTACTCATCTCAGAGAAAGTCTG6CACCCCTGTGTCCAGACGAC 673
Db 610 TTCACTCTTCAAGTGTACTCATCTCAGAGAAAGTCTG6CACCCCTGTGTCCAGACGAC 669
QY 674 TGGAAACGAACTACGGGCGGGGCGCTGACAGGACATGGGCTATAAGATAATTTTAC 733
Db 670 TGGAAACGAACTACGGGCGGGGCGCTGACAGGACATGGGCTATAAGATAATTTTAC 729
QY 734 TCTAGCCAAAGAAATGTGATGATGACAGGAGATCCACAGCTTTATGAACTGAAACAGT 793
Db 730 TCTAGCCAAAGAAATGTGATGATGACAGGAGATCCACAGCTTTATGAACTGAAACAGT 789
QY 794 GCCGGCAATGTGATATCTATAAAAAACTGTACACAGTATGCTGTCTTCAAAAGCA 853
Db 790 GCCGGCAATGTGATATCTATAAAAAACTGTACACAGTATGCTGTCTTCAAAAGCA 849
QY 854 GTGTTTCTTACGCTGTATAGCCGCGGGGTCAACTTGAACCTCAAGCCGACGAGCAG 913
Db 850 GTGTTTCTTACGCTGTATAGCCGCGGGGTCAACTTGAACCTCAAGCCGACGAGCAG 909
QY 914 ATCGTGGCGGCGAGAGCGGCTCCCGGGGGCTGGCCCTGGGCGGTGACGCTCAGCT 973
Db 910 ATTTGGGGCGGCGAGAGCGGCTCCCGGGGGCTGGCCCT-66CAGGTGACGCTGACGT 968
QY 974 CCAGAACGTCCACGCTGTGCGGAGGCTCCATCATACCCCGAGTGGATCTGACAGCCGC 1033
Db 969 CCAGAACGTCCACGCTGTGCGGAGGCTCCATCATACCCCGAGTGGATCTGACAGCCGC 1028
QY 1034 CCACCTGCTGGAAAAAACCCTTTAACAATCCATGGGATTTGGGCGGATTTT 1093
Db 1029 CCACCTGCTGGAAAAAACCCTTTAACAATCCATGGGATTTGGGCGGATTTT 1088
QY 1094 GAGACAACTCTTCAATGTTCTATGAGCCGAGATACCAAGTAGAAAAAGTATTCATCC 1153
Db 1089 GAGACAACTCTTCAATGTTCTATGAGCCGAGATACCAAGTAGAAAAAGTATTCATCC 1148
QY 1154 AAATATATGACTCAAGACCAAGAACATGACATTTGCGGTGATGAAGCTGACAGAGCCTCT 1213
Db 1149 AAATATATGACTCAAGACCAAGAACATGACATTTGCGGTGATGAAGCTGACAGAGCCTCT 1208
QY 1214 GACTTTCAACGACCTAGTGAAGAACAGTGTGTGCTGCCCAACCAGGATGATCTGACGCC 1273
Db 1209 GACTTTCAACGACCTAGTGAAGAACAGTGTGTGCTGCCCAACCAGGATGATCTGACGCC 1268
QY 1274 AGAACAGCTGTGCTGATTTCCGGGTGGGGGCGACCGAGGAAAGGAAACCTCAGA 1333
Db 1269 AGAACAGCTGTGCTGATTTCCGGGTGGGGGCGACCGAGGAAAGGAAAGTCTCAGA 1328
QY 1334 AGTGTGACAGCTGCGCAAGGTCTTCTCATTTGAGACACAGAGATCAACAGCAGATATGT 1393
Db 1329 AGTGTGACAGCTGCGCAAGGTCTTCTCATTTGAGACACAGAGATCAACAGCAGATATGT 1388
QY 1394 CTATGACAACTGATCAACACAGCCATATCTGTGCGGCTTCTGACAGGGGAAAGTCTGA 1453
Db 1389 CTATGACAACTGATCAACACAGCCATATCTGTGCGGCTTCTGACAGGGGAAAGTCTGA 1448
QY 1454 TTCTTGGCAGGGTGACATGAGAGGCGCTGAGTCACTTGAAGAACAAATATCTGGTGGCT 1513
Db 1449 TTCTTGGCAGGGTGACATGAGAGGCGCTGAGTCACTTGAAGAACAAATATCTGGTGGCT 1508
QY 1514 GATAGGGATACAAAGCTGGGCTTCTGGCTGTGCCAAAGCTTACAGACCAAGAGTACGG 1573
Db 1509 GATAGGGATACAAAGCTGGGCTTCTGGCTGTGCCAAAGCTTACAGACCAAGAGTACGG 1568
QY 1574 GAATGTGATGATTTACAGGAGCTGATTTATGACAAATGAGGCGAGCGCTAATCCAC 1633
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Db 1569 GAATGTGATGATTTACAGGAGCTGATTTATCGACAAATGAGGCGAGCGGCTAATCCAC 1628
QY 1634 ATGTCCTTGTGCTTGTACAGCTGCTTTTACAAAGAAACAAATGGGCGTGGTTTGTCCCGC 1693
Db 1629 ATGTCCTTGTGCTTGTACAGCTGCTTTTACAAAGAAACAAATGGGCGTGGTTTGTCCCGC 1688
QY 1694 TGCATGATTTACTCTTAGAGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGAAT 1753
Db 1689 TGCATGATTTACTCTTAGAGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGAAT 1748
QY 1754 TGTGTGCTTTGGCACTCTCTGCAATCTGTGTGACAGGCTGACGTGCTCCCTGCCAGCC 1813
Db 1749 TGTGTGCTTTGGCACTCTCTGCAATCTGTGTGACAGGCTGACGTGCTCCCTGCCAGCC 1808
QY 1814 TGCCTCCCTTACCCCTTGTCCGCAAGGGGTATGAGCGGCTGGTGTGGGCACTGGCG 1873
Db 1809 TGCCTCCCTTACCCCTTGTCCGCAAGGGGTATGAGCGGCTGGTGTGGGCACTGGCG 1868
QY 1874 TCAAGTGTGAGAGAGAGGGGTGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCCCTTC 1933
Db 1869 TCAAGTGTGAGAGAGAGGGGTGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCCCTTC 1928
QY 1934 CAGGGGCCAATTTTGGATGATGATGAGAGTGTACCTCTCAGCTGCTGGATGACTTGACA 1993
Db 1929 CAGGGGCCAATTTTGGATGATGATGAGAGTGTACCTCTCAGCTGCTGGATGACTTGAGA 1988
QY 1994 TGAAGAGAGAGACATGGAAGAGAGAGACAGCAGGCTGACCTGACAGCGGCTG-CCCTCT 2052
Db 1989 TGAAGAGAGAGACATGGAAGAGAGAGACAGCAGGCTGACCTGACAGCGGCTGACCTCT 2048
QY 2053 GGGGCCACTTGTGATGTGCCAGAGCTTACCTCTCCAAAGGGGATTTTCTGATGGGTTTC 2112
Db 2049 GGGGCCACTTGTGATGTGCCAGAGCTTACCTCTCCAAAGGGGATTTTCTGATGGGTTTC 2108
QY 2113 TTAGAGCCTTACAGAGCCCTGATGTGTGCGCAGAAATAAGGGGACCAAGCCCTTATGGGTG 2172
Db 2109 TTAGAGCCTTACAGAGCCCTGATGTGTGCGCAGAAATAAGGGGACCAAGCCCTTATGGGTG 2168
QY 2173 GTGACGTGTGATGACCTTGTGAAGGGGAAACAGAAATTTTGTCTTATGGGCTAGAA 2232
Db 2169 GTGACGTGTGATGAC-CTTGTGAAGGGGAAACAGAAATTTTGTCTTATGGGCTAGAA 2227
QY 2233 TATAGACATGCCCCCTTGGGTGCGAGGAAACAAATTGAAAAAGAACTTGCCCTGACATC 2292
Db 2228 TATAGACATGCCCCCTT-GGTGGAGGGGAAACAAATTGAAAAAGAACTTGCCCTGACATC 2286
QY 2293 CTGCTGACAGTCTCCACCTGACATTTGGGTGGGCTCTGGGAGGAGACACTAGCCTTCC 2352
Db 2287 CTGCTGACAGTCTCCACCTGACATTTGGGTGGGCTCTGGGAGGAGACACTAGCCTTCC 2346
QY 2353 TCCCTATCTCCCTGACCCCTGCTAGCACCCCTGAGAGGTGACATGGCCCTTGGTCC 2412
Db 2347 TCCCTATCTCCCTGACCCCTGCTCTAGCACCCCTGAGAGGTGACATGGCCCTTGGTCC 2406
QY 2413 GGGCAGGGGCGCAAGTGTGGACACATGTTGGCTTTCAGGCGCTGATGACTGGAAA 2472
Db 2407 GG--CAGGGCGGCAAGTGTGGACACATGTTGGCTTTCAGGCGCTGATGACTGGAAA 2464
QY 2473 TTGAGGTCCATGGGGGAAATCAAGGATGCTCACTTAAAGTACACTGTTTCCATGTTATG 2532
Db 2465 TTGAGGTCCATGGGGGAAATCAAGGATGCTCAAGTAAAGTACACTGTTTCCATGTTATG 2524
QY 2533 TTCTTACAACTTGTACCTCAGTGTGCTGCGGAAACTTGTGATGTCTCCAAATGAT 2592
Db 2525 TTCTTACAACTTGTACCTCAGTGTGCTGCGGAAACTTGTGATGTCTCCAAATGAT 2584
QY 2593 CCACCTTCAATTTAACTCTTGAAGTATCATCTTTGGCAAGTAAAGAGTGGTGGCTAT 2652
Db 2585 CCACCTTCAATTTAACTCTTGAAGTATCATCTTTGGCAAGTAAAGAGTGGTGGCTAT 2644
QY 2653 TTACAGTGTGTGACAAATAAGTGGCTCTGACTTAACGTTCTATAATGAATGTGCTG 2712
Db 2645 TTACAGTGTGTGACAAATAAGTGGCTCTGACTTAACGTTCTATAATGAATGTGCTG 2704
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Db 1200 TGCAGAACCTCTGACTTTCACAGCACTAGTAAACCACTGTGTCTGCCCAACCCAGGCA 1259
Qy 1261 TGATGCTGCAGCCAGACAGACTCTGTGATTTCCGGGTGGGGGCGCCACGAGAGAAAG 1320
Db 1260 TGATGCTGCAGCCAGACAGACTCTGTGATTTCCGGGTGGGGGCGCCACGAGAGAAAG 1319
Qy 1321 GGAAGACCTCAGAAAGTGTGAACGCTGCCAAGGTGTCTTCATTGAGACACAGAGATGCA 1380
Db 1320 GGAAGACCTCAGAAAGTGTGAACGCTGCCAAGGTGTCTTCATTGAGACACAGAGATGCA 1379
Qy 1381 ACAGACAGATATGCTATGACAACTGATCACAACGACCATGATGTGCGGCTTCCTG 1440
Db 1380 ACAGACAGATATGCTATGACAACTGATCACAACGACCATGATGTGCGGCTTCCTG 1439
Qy 1441 AGGGGAAGCTGATTTCTTGCCAGGGGTGACAGTGAAGGGCTCTGTGCTACCTTCGAAACCA 1500
Db 1440 AGGGGAAGCTGATTTCTTGCCAGGGGTGACAGTGAAGGGCTCTGTGCTACCTTCGAAACCA 1499
Qy 1501 ATATCTGGTGGCTGATPAGGGGATACAAAGCTGGGGTTCTGGCTGTGCCAAAGCTTACACAC 1560
Db 1500 ATATCTGGTGGCTGATPAGGGGATACAAAGCTGGGGTTCTGGCTGTGCCAAAGCTTACACAC 1559
Qy 1561 CAGAGGTACAGGGAATGATGATTCACGAGACTGGATTTATGAGACAAATGAGGGGAG 1620
Db 1560 CAGAGGTACAGGGAATGATGATTCACGAGACTGGATTTATGAGACAAATGAGGGGAG 1619
Qy 1621 ACGGCTAAATCCACATGATGCTTCGCTGACCTGCTTTTACAAAGAAACATGAGGGCTG 1680
Db 1620 ACGGCTAAATCCACATGATGCTTCGCTGACCTGCTTTTACAAAGAAACATGAGGGCTG 1679
Qy 1681 TTTTCTTCCCTCCGCTGATGATTTACTCTTAGAGATGATTCAGAGTCACTTCAATTTTAT 1740
Db 1680 TTTTCTTCCCTCCGCTGATGATTTACTCTTAGAGATGATTCAGAGTCACTTCAATTTTAT 1739
Qy 1741 TAAACAGTGAATTTCTGCTGCTTTGGACCTCTGTCATTTCTGTGAGGCTCAGAGGCT 1800
Db 1740 TAAACAGTGAATTTCTGCTGCTTTGGACCTCTGTCATTTCTGTGAGGCTCAGAGGCT 1799
Qy 1801 CCCCTGCCAGCCTCTCTCCCTAACCCCTTGTCCGCAAGGGGTGATGAGCCGGCTGTTG 1860
Db 1800 CCCCTGCCAGCCTCTCTCCCTAACCCCTTGTCCGCAAGGGGTGATGAGCCGGCTGTTG 1859
Qy 1861 TGGGCACTGGGGGTCAAGTGTGAGAGAGAGGGGTGAGGCTCCCATTTGAAATCTTCT 1920
Db 1860 TGGGCACTGGGGGTCAAGTGTGAGAGAGAGGGGTGAGGCTCCCATTTGAAATCTTCT 1919
Qy 1921 GCTGATCCTTCCAGGGGGCAATTTTGGATGAGCATGGAGGTGACCTCAGTGTGT 1980
Db 1920 GCTGATCCTTCCAGGGGGCAATTTTGGATGAGCATGGAGGTGACCTCAGTGTGT 1979
Qy 1981 GGATGACTTGAAGTAAAGAGAGAGACATGGAAGGAGAGACAGCCAGGTGACCTGCA 2040
Db 1980 GGATGACTTGAAGTAAAGAGAGAGACATGGAAGGAGAGACAGCCAGGTGACCTGCA 2039
Qy 2041 GCGGCTG-CCTCTGGGGCCACTTGGTGTGTCGCCAGCCTTCCACAAAGGGATTT 2099
Db 2040 GCGGCTG-CCTCTGGGGCCACTTGGTGTGTCGCCAGCCTTCCACAAAGGGATTT 2099
Qy 2100 TGGCTATGGGTTCTTAGAGCCTTAGACGCCCTGATGCTGGGCAAGAAATTAAGGACCG 2159
Db 2100 TGGCTATGGGTTCTTAGAGCCTTAGACGCCCTGATGCTGGGCAAGAAATTAAGGACCG 2159
Qy 2160 CCTTCATGGGTGTGAGCTGTGATTCACCTTGAAGGGGAGACAAATTTTGTCT 2219
Db 2160 CCTTCATGGGTGTGAGCTGTGATTCACCTTGAAGGGGAGACAAATTTTGTCT 2218
Qy 2220 TATGGGGTGAATATAGACAGTGGCTTGGGTGAGGGGAGCAATTTGAAAGAACTT 2279
Db 2219 TATGGGGTGAATATAGACAGTGGCTTGGGTGAGGGGAGCAATTTGAAAGAACTT 2277
Qy 2280 GCCCTGAGACACTCCTGCTGAGGCTGCTCCACCTGACATTTGGGTGGGCTCCCTGGAGGGA 2339
Db 2278 GCCCTGAGACACTCCTGCTGAGGCTGCTCCACCTGACATTTGGGTGGGCTCCCTGGAGGGA 2337

Qy 2340 GACTAGCCTTCTCTCTCATCTCTGACCCCTGTCTAGACCCCTGGAGACTGCACAT 2399
Db 2338 GACTAGCCTTCTCTCTCATCTCTGACCCCTGTCTAGACCCCTGGAGACTGCACAT 2397
Qy 2400 GCCCTTGGTCTCTGGGCGAGGGGCGCCAAAGTGTGGACACATGTTGGCTTTCAGGCTGC 2459
Db 2398 GCCCTTGGTCTCTGGGCGAGGGGCGCCAAAGTGTGGACACATGTTGGCTTTCAGGCTGC 2455
Qy 2460 TAGTCACTGAAATTTAGGTTCCATGGGGGAA 2490
Db 2456 TAGTCACTGAAATTTAGGTTCCATGGGGGAA 2486

RESULT 8
US-10-012-896-894
Sequence 894, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocke, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Manfande, Yoshinori
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 894
LENGTH: 2479
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-894

Query Match 67.1%; Score 2309.4; DB 9; Length 2479;
Best Local Similarity 98.6%; Pred No. 0;
Matches 2425; Conservative 0; Mismatches 21; Indels 13; Gaps 9;

Qy 93 GTCATATGAACATTCACATACCTATCTATCTGATGCTGTGATTAACAGCAAGATG 152
Db 1 GTCATATGAACATTCACATACCTATCTATCTGATGCTGTGATTAACAGCAAGATG 60
Qy 153 CTTTGAACACAGGTTACACACAGCTATTTGAGCTTACTATGAAACCATGATATACAC 212
Db 61 CTTTGAACACAGGTTACACACAGCTATTTGAGCTTACTATGAAACCATGATATACAC 120
Qy 213 CGAAACCCCTATCCCGACAGACCCACATGTGCTCCCATGCTGAGAGGTGATCCGG 272
Db 121 CGAAACCCCTATCCCGACAGACCCACATGTGCTCCCATGCTGAGAGGTGATCCGG 180
Qy 273 CTCAGTACACCCGTCGCCGCTGCCAGTAGCCGCCGAGGGTCTGACGAGGCTTCCA 332

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Db 181 CTCAGTACTACCCCTCCCGCGGCCCCAGTACGCCCGGAGGGTCTTGACGAGGCTTCCA 240
QY 333 ACCCGGTGTCGACGACGAGCCCAATCCCATCCGGAGACAGTGTGACCTCAAGACTA 392
Db 241 ACCCGGTGTCGACGACGAGCCCAATCCCATCCGGAGACAGTGTGACCTCAAGACTA 300
QY 393 AGAAGACCTGTGATCATTGACCTTGACCCCTGGGACCTTCTGTGGAGCTGCGTGGCG 452
Db 301 AGAAGACCTGTGATCATTGACCCCTGGGACCTTCTGTGGAGCTGCGTGGCG 360
QY 453 CTGGCTACTCTGGAGTGTGAGGAGCAGTGTGACAGTGTGACAGTGTGACAGTGTGAC 512
Db 361 CTGGCTACTCTGGAGTGTGAGGAGCAGTGTGACAGTGTGACAGTGTGACAGTGTGAC 420
QY 513 CCTGAGTACTGTGATCAACCCCTCTAACTGTGTGATGAGGCTGTGACAGTGTGACAG 572
Db 421 CCTGAGTACTGTGATCAACCCCTCTAACTGTGTGATGAGGCTGTGACAGTGTGACAG 480
QY 573 GGGAGGAGAGATCGGTGTGCTGCTGACGAGCAGCAAACTTCACTTCAAGGTACT 632
Db 481 GGGAGGAGAGATCGGTGTGCTGCTGACGAGCAGCAAACTTCACTTCAAGGTACT 540
QY 633 CATCTCAGAGAGATCCCTGGGACCCCTGTGTGCTGACAGAGACAGTGTGAGAGAGAG 692
Db 541 CATCTCAGAGAGATCCCTGGGACCCCTGTGTGCTGACAGAGACAGTGTGAGAGAGAG 600
QY 693 GGGGCGCTGACGAGGACATGGGCTATAGATATATTTTACTTACCCAGAGATAGTG 752
Db 601 GGGGCGCTGACGAGGACATGGGCTATAGATATATTTTACTTACCCAGAGATAGTG 660
QY 753 ATGACAGGAGATCCACAGCTTTATGAACATGAACACAAATGCGGCAATGCTATCT 812
Db 661 ATGACAGGAGATCCACAGCTTTATGAACATGAACACAAATGCTATCTGCTATCT 720
QY 813 ATAAAAACCTGTACACAGTATGCTGTCTTCAAAAGAGTGGTTCTTAGCGTGA 872
Db 721 ATAAAAACCTGTACACAGTATGCTGTCTTCAAAAGAGTGGTTCTTAGCGTGT 780
QY 873 TAGCCTGGGGGTCACCTTGAATCAACCCGACAGAGAGATGCTGGGCGGACGAGACG 932
Db 781 TAGCCTGGGGGTCACCTTGAATCAACCCGACAGAGAGATGCTGGGCGGAGAGACG 840
QY 933 CGCTCCCGGGGCTGGGCTGTGGAGGTGACGCTGACGCTCAGAGAGTCCAGCTGTGC 992
Db 841 CGCTCCCGGGGCTGGGCTGTGGAGGTGACGCTGACGCTCAGAGAGTCCAGCTGTGC 899
QY 993 GGAGGCTCAGTATCAGCCCGGAGTGGATGGTGAACGCGGCACTGGTGGAAAACT 1052
Db 900 GGAGGCTCAGTATCAGCCCGGAGTGGATGGTGAACGCGGCACTGGTGGAAAACT 959
QY 1053 CTTAAACATCCATGGCATTTGAGCGGATTTGCGGGATTTTGAAGCATCTTCACTGTC 1112
Db 960 CTTAAACATCCATGGCATTTGAGCGGATTTGCGGGATTTTGAAGCATCTTCACTGTC 1019
QY 1113 TATGAGCGCGGATACCAAGTATGAAGAAAGTATTTCTCATCCAAATTTAGCTCCAGAC 1172
Db 1020 TATGAGCGCGGATACCAAGTATGAAGAAAGTATTTCTCATCCAAATTTAGCTCCAGAC 1079
QY 1173 AAGAACAATGACATTTGGCTGATGAAGTGTGAGAAAGCTGTGACATTTTCAAGCACTATG 1232
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QY 1233 AAACAGTGTGTGCTCCCAACCCAGGCAATGATGTGACAGCAGAAACAGCTGTGCTGAT 1292
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QY 1293 TCGGGGTGGGGGCGCACCGAGAGAAAGGAGAAAGTCTGAGAGTGTGACAGCTGTGCAAG 1352
Db 1200 TCGGGGTGGGGGCGCACCGAGAGAAAGGAGAAAGTCTGAGAGTGTGACAGCTGTGCAAG 1259
QY 1353 GTGCTTCTCATTTGAGACACAGATGCAAGAGATGTGCTATGACAACTGATCA 1412
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Db 1260 GTGCTTCTCATTTGAGACACAGATGCAAGAGATGTGCTATGACAACTGATCA 1319
QY 1413 CCAGCATGATGTGTGCGCGCTTCTGCGAGGAGAAAGTGTGCTTGTGCGAGGATGACAGT 1472
Db 1320 CCAGCATGATGTGTGCGCGCTTCTGCGAGGAGAAAGTGTGCTTGTGCGAGGATGACAGT 1379
QY 1473 GGAGGCGCTGTGTGCTTGTGAGAAACATATCTGTGTGTGATAGGGATACAGCTGG 1532
Db 1380 GGAGGCGCTGTGTGCTTGTGAGAAACATATCTGTGTGTGATAGGGATACAGCTGG 1439
QY 1533 GGTGTGCTGTGCGCAAGCTTACAGACAGAGAGTGTGCGGAGTGTGATGTATTCAG 1592
Db 1440 GGTGTGCTGTGCGCAAGCTTACAGACAGAGAGTGTGCGGAGTGTGATGTATTCAG 1499
QY 1593 GACTGATTTATGCAATATAGGAGAGAGCTATATCCATGATGCTTGTGCTGACG 1652
Db 1500 GACTGATTTATGCAATATAGGAGAGAGCTATATCCATGATGCTTGTGCTGACG 1559
QY 1653 TCGTTTTCAAGAAACAAATGGGCTGTGCTTCCCGTGCATGATTTACTTTAGA 1712
Db 1560 TCGTTTTCAAGAAACAAATGGGCTGTGCTTCCCGTGCATGATTTACTTTAGA 1619
QY 1713 GATGATTCAGAGTCTACTTATTTTATTAACAGTGAAGTGTGCTGTGCTGACACT 1772
Db 1620 GATGATTCAGAGTCTACTTATTTTATTAACAGTGAAGTGTGCTGTGCTGACACT 1679
QY 1773 CTGCCATCTGTGACGAGTGTGAGTGTGCTGCTGCCAGCTGCTTCCCTAACCCCTTG 1832
Db 1680 CTGCCATCTGTGACGAGTGTGAGTGTGCTGCTGCCAGCTGCTTCCCTAACCCCTTG 1739
QY 1833 TCCGCAAGGGGTGATGCGCGCTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1890
Db 1740 TCCGCAAGGGGTGATGCGCGCTGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1799
QY 1891 GGGTGGAGGCTG--CCCATGAGATCTTCTGCTGAGTCTTCCAGGAGGCAATTTGG 1949
Db 1800 GGGTGGAGGCTGCGCCCATGAGATCTTCTGCTGAGTCTTCCAGGAGGCAATTTGG 1859
QY 1950 ATGAGCATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2009
Db 1860 ATGAGCATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1919
QY 2010 TGGAAAGGAGACAGCCAGTGTGACCTGACAGCGGCTG--CCTGTGGGCGCACTTGTGT 2068
Db 1920 TGGAAAGGAGACAGCCAGTGTGACCTGACAGCGGCTG--CCTGTGGGCGCACTTGTGT 1979
QY 2069 GTCGCCAGCTTACCTTCTGCAAGAGGAGTGTGCTGAGTGTGCTTGAAGCTTACAGCAG 2128
Db 1980 GTCGCCAGCTTACCTTCTGCAAGAGGAGTGTGCTGAGTGTGCTTGAAGCTTACAGCAG 2036
QY 2129 CCTGATGCTGCGCAAGATTAAGGAGACAGCCCTTCAATGGGTGTGACGTGTGATCAG 2188
Db 2037 CCTGATGCTGCGCAAGATTAAGGAGACAGCCCTTCAATGGGTGTGACGTGTGATCAG 2095
QY 2189 CTTGTAGGGAGACAGAAATTTTGTCTTATGGGTGTGAGATATAGACATGCGCTT 2248
Db 2096 CTTGTAGGGAGACAGAAATTTTGTCTTATGGGTGTGAGATATAGACATGCGCTT 2155
QY 2249 GGGTGGAGGAGACAAATTTGAAGAGAACTGCTGAGCACTGCTGTGAGAGTGTGCA 2308
Db 2156 GGGTGGAGGAGACAAATTTGAAGAGAACTGCTGAGCACTGCTGTGAGAGTGTGCA 2214
QY 2309 CCTGCAATTTGGGTGGGCTCTGTGAGAGAGACATGCTTCCATCTGCTGCTGCA 2368
Db 2215 CCTGCAATTTGGGTGGGCTCTGTGAGAGAGACATGCTTCCATCTGCTGCTGCA 2274
QY 2369 CCTGCTCTAGCAACCTGAGAGTGTGACATGCTTGTGCTGTGAGAGAGGAGGCGCAAG 2428
Db 2275 CCTGCTCTCTAGCAACCTGAGAGTGTGACATGCTTGTGCTGTGAGAGAGGAGGCGCAAG 2331
QY 2429 TCTGGACACATGTGCTCTTCAAGGCTGCTATGCTGCAAAATTTGAGTGTGATGAGG 2488
Db 2332 TTTGGACACATGTGCTCTTCAAGGCTGCTATGCTGCAAAATTTGAGTGTGATGAGG 2391
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[illegible]

RESULT 9

US-09-895-793-894
; Sequence 894, Application US/09895793

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Harlocker, Susan L.

APPLICANT: JIANG, YUQIU

APPLICANT: Kalos, Michael D

APPLICANT: Retter, Marc W.

APPLICANT: STOLK, John A.
APPLICANT: Day, Craig H.

APPLICANT: Vedwick, Thomas

APPLICANT: Carter, Darrick

APPLICANT: L1, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skelky, Yassil

APPLICANT: Henderson, Robert

APPLICANT: Hural, John

APPLICANT: McNeill, Patricia D.

APPLICANT: Houghton, Raymond L.

APPLICANT: Foy, Teresa

APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF...

TITLE OF INVENTION: DIS

FILE REFERENCE: 210121.5340
CURRENT APPLICATION NUMBER:

; CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 982

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; SOFTWARE: FastSeq for Windows Version 3.0.0
; SEQ ID NO 804
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; SEQ ID NO 894
:
: LENGTH: 2479

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LENGTH: 2475
TYPE: DNA

ORGANISM: Homo sapiens

US-09-895-793-89

Answer: Match

Query Mail
Rest Tools

best local climatology
Matches 2425; Conservat

QY 93 GTC

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DD 1 01C1M110TACM11CC6GAIAC1M1CMI1AC1C6

Qy	153	CTTGAACCTAGGGGTCACACACACACTATTGGACCTTACTCTATGAAACCAATGATATACAC	212
Db	61	CTTTGAACCTAGGGTCACACACACACTATTTGGACCTTACTCTATGAAACCAATGATATACAC	120
Qy	213	CGGAAACCCCTATTCGCCGACACAGCCCACTGTGTGCCACTGTCTACAGAGTGATCCGG	272
Db	121	CGGAAACCCCTATTCGCCGACACAGCCCACTGTGTGCCACTGTCTACAGAGTGATCCGG	180
Qy	273	CTCAGTACTACCGGTCCCGCGTGGCCCAAGTACAGCCCGGAGGGTCCATACGACAGGCTTCCA	332
Db	181	CTCAGTACTACCGGTCCCGCGTGGCCCAAGTACAGCCCGGAGGGTCCATACGAGGCTTCCA	240
Qy	333	ACCCGCTGTGCACGACGAGCCCAATCCCATCCGGGACAGTGTGACCTCTCAAGACTA	392
Db	241	ACCCGCTGTGCACGACGAGCCCAATCCCATCCGGGACAGTGTGACCTCTCAAGACTA	300
Qy	393	AGAAAGCACTGTGCATCACTTTGACCTCGGGGACCTTCTCTGTGTGGACGTGCCTGGCCG	452
Db	301	AGAAAGCACTGTGCATCACTTTGACCTCGGGGACCTTCTCTGTGTGGACGTGCCTGGCCG	360

OY	453	CTGGCTACTCTGGAAGTCTATGSGGACGAAAGTGCCTCCAACTCTGGATAGAGTCCACT	512
Db	361	CTGGCCCTACTCTGGAAAGTTATGGGACGAAAGTGCCTCAACTCTGGATAGAGTCCGACT	420
OY	513	CCTGAGGTACTGATCAACCCCTCAACCTGGGTATGATGGCGTGCACACTGCCCCGGCG	572
Db	421	CCTGAGGTACTGATCAACCCCTCTTAAGTGGTGTATGGCTGTGCACACTGCCCCGGCG	480
OY	573	GGGAGACGAGAAATCGGTGTGTTCGGCTCTACGGACCAAACTTCCTTCAAGTGTACT	632
Db	481	GGGAGACGAGAAATCGGTGTGTTCGGCTCTACGGACCAAACTTCCTTCAAGTGTACT	540
OY	633	CATCTCAGAGGAAGTCTGTGGCACCCCTGTGTGCCAAGACACTTGGAAACGAACCTACGGGC	692
Db	541	CATCTCAGAGGAAGTCTGTGGCACCCCTGTGTGCCAAGACACTTGGAAACGAACCTACGGGC	600
OY	693	GGGGGCGCTCGAGGAGCATGGGCTATTAAGAAATATTTTACTGTAGCCAAAGAAATAGGG	752
Db	601	GGGGGCGCTCGAGGAGCATGGGCTATTAAGAAATATTTTACTGTAGCCAAAGAAATAGGG	660
OY	753	ATGACAGCGGATCCACCAAGCTTTATGAAACTGAACAAGTCCCGGCAATGTGCATATCT	812
Db	661	ATGACAGCGGATCCACCAAGCTTTATGAAACTGAACAAGTCCCGGCAATGTGCATATCT	720
OY	813	ATTAATAACTGTACCAAGATGATGCTGTCTTCAAAAAGCATGTGTCTTTAGCTGTATA	872
Db	721	ATTAATAACTGTACCAAGATGATGCTGTCTTCAAAAAGCATGTGTCTTTAGCTGTATA	780
OY	873	TAGCCTCGGGGATCAATTAACTCAAGCCCGCAGAGCAGATCGTGGGCGGCGAGAGCG	932
Db	781	TAGCCTCGGGGATCAATTAACTCAAGCCCGCAGAGCAGATCGTGGGCGGCTGAGAGCG	840
OY	933	CGCTCCCGGGGCGCTGGCCCTGGGCGAGGTCAGCTTCACCTCCAGAACGCTCCACGTGTGC	992
Db	841	CGCTCCCGGGGCGCTGGCCCT - GGCAGGTCAGCTTCACGTCAGAACGCTCCACGTGTGC	899
OY	993	GGAGGCTCCATCAATCAACCCCGAGGTGATGTACAGCCGCCCATCGGTGGTAAAAACT	1052
Db	900	GGAGGCTCCATCAATCAACCCCGAGGTGATGTACAGCCGCCCATCGGTGGTAAAAACT	959
OY	1053	CTTAACAATCCATGCAATGGATGGAGCGCATTTGCGGGGATTTTGAGAACAACTTTCAATGTC	1112
Db	960	CTTAACAATCCATGCAATGGATGGAGCGCATTTGCGGGGATTTTGAGAACAACTTTCAATGTC	1019
OY	1113	TATGGAGCCGGATACCAAGTAGAAAAAGTATTTCTCATCCAAATTAATGATCTCCAAAGCC	1172
Db	1020	TATGGAGCCGGATACCAAGTAGAAAAAGTATTTCTCATCCAAATTAATGATCTCCAAAGCC	1079
OY	1173	AAGAAACAATGCAATTTGGGTGATGAAGAGTCCCAAAACCTCTCACTTTCAAGCAACTACTG	1232
Db	1080	AAGAAACAATGCAATTTGGGTGATGAAGAGTCCCAAAACCTCTCACTTTCAAGCAACTACTG	1139
OY	1233	AAACCAAGTGTGTCTGCCCAACCCAGGCATGATCTCAGCCAGAACAGTCTGTGTGATT	1292
Db	1140	AAACCAAGTGTGTCTGCCCAACCCAGGCATGATCTCAGCCAGAACAGTCTGTGTGATT	1199
OY	1293	TCCGGGTGGGGGCCACCGAGAGAAAGGAGAGACTCAAGAAATGCTGAACGCTGCCAAG	1352
Db	1200	TCCGGGTGGGGGCCACCGAGAGAAAGGAGAACCTCAGAAAGTCTGAACGCTGCCAAG	1259
OY	1353	GTGCTTCATTTGAGACAGAGATGTGCACAGAGATATGTCTATGACAAACCTGATACAA	1412
Db	1260	GTGCTTCATTTGAGACAGAGATGTGCACAGAGATATGTCTATGACAAACCTGATACAA	1319
OY	1413	CCAGCAATGATCTGTGCCGGCTTCTGTCAGAGGAAAGTGTGATCTCTTCCAGGGGTACAGT	1472
Db	1320	CCAGCAATGATCTGTGCCGGCTTCTGTCAGAGGAAAGTGTGATCTCTTCCAGGGGTACAGT	1379
OY	1473	GGAGGGCTCTGGTCACTTTGAAAGAACATATTTGGTGGCTGATAGGGGATACAAAGCTGG	1532
Db	1380	GGAGGGCTCTGGTCACTTTGAAACAAACAAATATTTGGTGGCTGATAGGGGATACAAAGCTGG	1439

QY	1533	GGTCTTGGCTGCTCCAAAGCTTTCACACAGAGAGTACGGGAAATGTAATGGTATTACAG	15922
Db	1440	GGTTCTGGCTGTGGCCAAAGCTTTCACACAGAGAGTACGGGAAATGTAATGGTATTACAG	14939
QY	1593	GACTGCATTTATTCAGCAAAATGAGGCGAGACGGCTAAATCCATGGTCTTTCGTTGACG	16522
Db	1500	GACTGCATTTATTCAGCAAAATGAGGCGCAAAAGGGCTAATCCATGGTCTTTCGTTGACG	1559
QY	1553	TTCGTTTACAGAAACAAATGGGGCGTGTGGTTCCTCCCGTGACAGTAATTAATCTTAGA	17122
Db	1560	TTCGTTTACAGAAACAAATGGGGCGTGTGGTTCCTCCCGTGACAGTAATTAATCTTAGA	1619
QY	1713	GATGATTACAGAGTCACTTCATTTTATTTAAACAGTAAGAACTGTGTGGCTTTCGACACT	17722
Db	1620	GATGATTACAGAGTCACTTCATTTTATTTAAACAGTAAGAACTGTGTGGCTTTCGACACT	1679
QY	1773	CTGCCAATTCTGTGACAGGCTGTGACGTGGCTCCCTGCCACGCTGTCTCCCTAACCCCTTG	18322
Db	1680	CTGCGCAATCTGTGACAGGCTGTGACGTGGCTCCCTGCCACGCTGTCTCCCTAACCCCTTG	1739
QY	1833	TTCGCAAGGGGTGATGGCCGGCGGTGTGGGACATGGGGGCAAGTGGGA - GGAAG	1890
Db	1740	TTCGCAAGGGGTGATGGCCGGCGGTGTGGGACATGGGGGCAAGTGGGA - GGAAG	1799
QY	1891	GGGTGGAGGCTG - CCCCATTGAGATCTTCCGTGTGAGTCTCTTCCAGGGGCCAATTTGG	1949
Db	1800	GGTTGGAGGCTGCCCCCAATTGAGATCTTCCGTGTGAGTCTCTTCCAGGGGCCAATTTGG	1859
QY	1950	ATGAGCATGTAGACTGTACCTCTACGCTGTGATGACTTGAATGAAAAAGAGACACA	2009
Db	1860	ATGAGCATGTAGAGTGTACCTCTACGCTGTGATGACTTGAATGAAAAAGAGAGACA	1919
QY	2010	TGCAAAAGGAGACAGCAGAGGTGGCACCTGCAGGGCTG - CCTGTGGGGCACTTGGTAGT	2068
Db	1920	TGCAAAAGGAGACAGCAGAGGTGGCACCTGCAGGGCTG - CCTGTGGGGCACTTGGTAGT	1979
QY	2069	GTCCCCAGCCTCTCTCCAAAGGGGATTTTGTGATGGGTCTTAGAGCCTTAGCAGC	2128
Db	1980	GTCCCCAGCCTTA - - - CTTCACAAAGGGGATTTTGTGATGGGTCTTAGAGCCTTAGCAGC	2036
QY	2129	CTGTGATGTGTGGCCAAATAAAGGGGACCAAGCCCTTCAATGGGTGGTGAATGTAGTAC	2188
Db	2037	CTGTGATGTGTGGCCAAATAAAGGGGACCAAGCCCTTCAATGGGTGGTGAATGTAGTAC -	2095
QY	2189	CTTGTAGGGGGAACAGAAATTTTGTCTTATGAGGGTGAATAATATAGACAGTCCCTT	2248
Db	2096	CTTGTAGGGGGAACAGAAATTTTGTCTTATGAGGGTGAATAATATAGACAGTCCCTT	2155
QY	2249	GGGTGGAGGGAAGCAATTGAAAAAGAACTTGCCCTGAGCACTCTGTGGTGCAGTCTCCA	2308
Db	2156	-GGTGGAGGGAAGCAATTGAAAAAGAACTTGCCCTGAGCACTCTGTGGTGCAGTCTCCA	2214
QY	2309	CTGTGCAATTGGGTGGGGGCTCCGTGGGAGGAGACATCAGCCTTCCTCATCTCCCTCGA	2368
Db	2215	CTGTGCAATTGGGTGGGGGCTCCGTGGGAGGAGACATCAGCCTTCCTCATCTCCCTCGA	2274
QY	2369	CCCTGTCTCTAGCAGCCTGTGAGAGTGCACATGCTCCCTTGTCTGTGGCAGGGGCGCAG	2428
Db	2275	CCCTGTCTCTAGCAGCCTGTGAGAGTGCACATGCTCCCTTGTCTGTGGCAGGGGCGCAG	2331
QY	2429	TCTGGCACCATGTTGGCCTCTTTCAGGCGCTGTAGTCACTGGAATATGAGTCCATGGGG	2488
Db	2332	TCTGGCACCATGTCGGCCTCTTTCAGGCGCTGTAGTCACTGGAATATGAGTCCATGGGG	2391
QY	2489	AAATCAAGATGCTCAAGTTTAAGCTGACACTGTGTTCCAGTTATGTTTCTACACATTTGCT	2547
Db	2392	AAATCAAGATGCTCAAGTTTAAGCTGACACTGTGTTCCAGTTATGTTTCTACACATTTGAT	2450

RESULT 10
US-09-895-814-894
; Sequence 894, Application US/09895814
; Publication No. US20020193296A1

```

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Panger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITL OF INVENTION: DIAGNOSTIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 894
LENGTH: 2479
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-894

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Query Match	Similarity	97.1%	Score 2309.4	DB 9	Length 2479
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Db	1	GTCAATATGAAACATTTCCAGATACCTTATCAATTCATCGATGCTGTTGTGATACAGCAAGATGG	60		
QY	153	CTTTGAACCTCAGGGTCACACACACAGCTATTGGACCTTACTATGAAAACCATGATACCAAC	212		
Db	61	CTTTGAACCTCAGGGTCACACACACAGCTATTGGACCTTACTATGAAAACCATGATACCAAC	120		
QY	213	CGGAAAAACCCCTATCCCGACAGCCCACTGGGGCCCCACATGCTATACGAGGTGCATCCGG	272		
Db	121	CGGAAAAACCCCTATCCCGACAGCCCACTGGGGCCCCACATGCTATACGAGGTGCATCCGG	180		
QY	273	CTCAGTACTACCCGTCGCCCGTGCGCCAGTACGCCGCCGAGGGTCTTACGCAGAGCTTCCA	332		
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QY	333	ACCCCGTGTGTGCACGACGACCCAAATCCCATTCGGGACAGTGTGCACCTCAAAAGCTA	392		
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QY	393	AGAAAGACATGTGATATCACTTGACCTGGGGACCTTCTCTGTGTGGAGCTGTGCGTGCCG	452		
Db	301	AGAAAGACATGTGATATCACTTGACCTTGCGGGACCTTCTCTGTGTGGAGCTGTGCGTGCCG	360		
QY	453	CTGGCCACTCTGGAACCTTATGCGGACGAAAGTGCCTCAACTCTCGGGATATGAGTGGCACT	512		
Db	361	CTGGCCACTCTGGAACCTTATGCGGACGAAAGTGCCTCAACTCTCGGGATATGAGTGGCACT	420		
QY	513	CTTCAGGTACTGTGATCAACCCCTCTTAAGTGTGTGATGTGCGTCACTACATGGCCCGCG	572		
Db	421	CTTCAGGTACTGTGATCAACCCCTCTTAAGTGTGTGATGTGCGTGTCACTACATGGCCCGCG	480		
QY	573	GGGAGGACGAAATCGGTGTGTTCGCCCTTACGAGACCAAACTTCATCTTACAGGTACT	632		

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Db 461 GGGAGGACGAGATGGTGTGTTCCCTCTACGAGCCAACTTCATCTTCAGATGTACT 540
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Db 661 ATGACAGGGGATCCACAGCTTATGAACCTAACAACAAGTCCGGCAATGTCGATATCT 720
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Db 900 GAGAGCTCATCATCACCCCGAGTGAATCGTACAGCCGCCACATGCTGGAAAAAACC 959
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OY 1653 TCGTTTACAGAAAAACAATGGGGCTGCTTTCCTCCCGTCATGATTTACTCTTACA 1712
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Db 1620 GATGATTCAGAGGTCACTTCAATTTTATTAACAGTGAACCTTGTGGCTTGGCACTCT 1679
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Db 1740 TCCGCAAGGGGTGATGGCCGGCTGTGGTGGACACTGGGGGTCAATGTGGAAGGAGAG 1799
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Db 1800 GGGTGGAGGCTGCCCCCATTTGAGATCTTCTGTGATGCTCTTCCAGGGGCAATTTTG 1859
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OY 2010 TGGAAAGGAGACAGCCAGTGGCACTGACAGGCGTG -CCTTGGGGCACCTTGGTATG 2068
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Db 2096 CTTGTAAGGGGAGAACAAACATTTTGTCTTATGAGGGTGAAGATATAGCACTGCCCTT 2155
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OY 2429 TCTGGCACATGTTGGCTCTTTCAGGCTGTGCTGACTGAGAAATTAAGAGTCCATGGGG 2488
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Db 2392 AATCAAGAGTGTCAATTAAGTACACTGTTTCCATGATTTATGTTTCTACACATGAT 2450
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RESULT 11
US-09-759-143-894
; Sequence 894, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaochun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiaang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Mang, Aljun
APPLICANT: Skeiky, Yasser A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 894
LENGTH: 2479
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-894

Query Match 67.1%; Score 2309.4; DB 10; Length 2479;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2425; Conservative 0; Mismatches 21; Indels 13; Gaps 9;

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DB 1200 TCCGGGTGGGGGCGCCAGGAGAGAAAGAAAGCTTGAAGTGTCTAAAGCTGTCCAG 1259
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DB 1320 CCAGCATGATCTGTGCGGCTTCTGTGAGGGGAAAGCTGTCTTGTGCGAGGGTACAGT 1379
QY 1473 GAGGCGCTGTGCTACTTCAAGAAACAATATCTGTGTGATGAGGGATTAAGAGTGG 1532
DB 1380 GAGGCGCTGTGCTACTTCAAGAAACAATATCTGTGTGATGAGGGATTAAGAGTGG 1439
QY 1533 GGTCTGTGCTGTCCAAAGCTTACAGACCAAGAGTGTACGGGAATGTGATGTATTCAG 1592
DB 1440 GGTCTGTGCTGTCCAAAGCTTACAGACCAAGAGTGTACGGGAATGTGATGTATTCAG 1499
QY 1593 GACTGATTTATGCAAAATAGGGGACAGCGGCAATGCAATGCTTCTGCTCCCTGACG 1652
DB 1500 GACTGATTTATGCAAAATAGGGGACAGCGGCAATGCAATGCTTCTGCTCCCTGACG 1559
QY 1653 TCGTTTTACAAGAAACAATGGGGCTGTGTTTTGCTTCCCGCTGATGATTAAGTGA 1712
DB 1560 TCGTTTTACAAGAAACAATGGGGCTGTGTTTTGCTTCCCGCTGATGATTAAGTGA 1619
QY 1713 GATGATTCAGAGGTCACTTATTTATTAACAGTGAATGTGTGCTTGGCACTCT 1772
DB 1620 GATGATTCAGAGGTCACTTATTTATTAACAGTGAATGTGTGCTTGGCACTCT 1679
QY 1773 CTGCAATCTGTGCAAGGTGTGAGTGGCTTCCCGCTGCGCTGTCTTCAACCCCTTG 1832
DB 1680 CTGCAATCTGTGCAAGGTGTGAGTGGCTTCCCGCTGCGCTGTCTTCAACCCCTTG 1739
QY 1833 TCCGCAAGGGGTGATGCGCGCTGTGTTGTGGGCACTGTGCGGTTCAAGTGTGA -- GGAAG 1890
DB 1740 TCCGCAAGGGGTGATGCGCGCTGTGTTGTGGGCACTGTGCGGTTCAAGTGTGA 1799
QY 1891 GGGTGGAGGCTG - CCCCATTGAGATCTTCTGTGAGTCTTCTCCAGGGGCCAAATTTGG 1949

Db 241 ACCCGCTGCTGCAAGCAGCCCAATCCCATCCGGACAGTGTACCTCAAAACCTA 300
Qy 393 AGAAAGCACTGTGCATCACCTTGACCCCTGGGACCTTCTCGTGGAGCTGCGCTGGCCG 452
Db 301 AGAAAGCACTGTGCATCACCTTGACCCCTGGGACCTTCTCGTGGAGCTGCGCTGGCCG 360
Qy 453 CTGGCTACTCTGGAAGTTCATGGGACAGAGTGTCTCAACTCTGGGATAGAGTGGACT 512
Db 361 CTGGCTACTCTGGAAGTTCATGGGACAGAGTGTCTCAACTCTGGGATAGAGTGGACT 420
Qy 513 CCTCAGTACCTGCATCAACCCCTCACTGATGGGCGGTGTACACTGCCCCGGCG 572
Db 421 CCTCAGTACCTGCATCAACCCCTCACTGATGGGCGGTGTACACTGCCCCGGCG 480
Qy 573 GGGAGACAGAGATCGGTGTGTCCCTCTACGGACCAACTTCATCTTCAAGTGTACT 632
Db 481 GGGAGACAGAGATCGGTGTGTCCCTCTACGGACCAACTTCATCTTCAAGTGTACT 540
Qy 633 CATCTCAGAGAAATCTGGGACCTGTGTGCCAAGACACTGGAACGAGAACTACGGCG 692
Db 541 CATCTCAGAGAAATCTGGGACCTGTGTGCCAAGACACTGGAACGAGAACTACGGCG 600
Qy 693 GGGCGGCGTGCAGGGACATGGGCTATAGAATATTTTACTCTAGCCAAAGAAATAGTG 752
Db 601 GGGCGGCGTGCAGGGACATGGGCTATAGAATATTTTACTCTAGCCAAAGAAATAGTG 660
Qy 753 ATGACAGCGGATCCACACACTTATGAACACTGAACAAGTGGCGGCAATGTGATATCT 812
Db 661 ATGACAGCGGATCCACACACTTATGAACACTGAACAAGTGGCGGCAATGTGATATCT 720
Qy 813 ATAAAACTGTACACAGTATGCTGTCTTCAAAAGCAAGTGTCTTTAAGCTGTGA 872
Db 721 ATAAAACTGTACACAGTATGCTGTCTTCAAAAGCAAGTGTCTTTAAGCTGTGTG 780
Qy 873 TAGCCGCGGGGTCAACTGAACTCAAGCGCGCAGAGAGAGATCGTGGGGGAGAGCG 932
Db 781 TAGCCGCGGGGTCAACTGAACTCAAGCGCGCAGAGAGAGATCGTGGGGGAGAGCG 840
Qy 933 GCGTCCCGGGGCGTGGCCCTGGGACAGTCAAGCTCAGCTCAGAACGTCCACGTGTGC 992
Db 841 GCGTCCCGGGGCGTGGCCCT--GGCAGGTCAAGCTCAGCTCAGAACGTCCACGTGTGC 899
Qy 993 GGAAGTTCATATCACCCCCAGTGGATCTGTACAGCGCGCCACTGCTGGAAAAACCT 1052
Db 900 GGAAGTTCATATCACCCCCAGTGGATCTGTACAGCGCGCCACTGCTGGAAAAACCT 959
Qy 1053 CTTAAACATCCATGGCATTTGAGCGGCAATTTGGGGATTTTGAGCAATCTTTCATGTC 1112
Db 960 CTTAAACATCCATGGCATTTGAGCGGCAATTTGGGGATTTTGAGCAATCTTTCATGTC 1019
Qy 1113 TATGAGCGCGATACCAAGTAGAAAAAGTATTTCTCATCCAAATATGACTCCAGAGC 1172
Db 1020 TATGAGCGCGATACCAAGTAGAAAAAGTATTTCTCATCCAAATATGACTCCAGAGC 1079
Qy 1173 AAGAACATGACATTTGCGTGTATGAAGCTGTACAGCTTTCATCAAGCTAGTG 1232
Db 1080 AAGAACATGACATTTGCGTGTATGAAGCTGTACAGCTTTCATCAAGCTAGTG 1139
Qy 1233 AAACAGTGTGTCTGCGCAACCCAGCATGATCTGACAGCAGAACAGCTCTCTGATTT 1292
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Qy 1293 TCCGGGTGGGGGCCACCGAGGAAGGAAGAACTCAGAAAGTGTGTAAGCTGTCCAG 1352
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Qy 1353 GTGCTTCTATGTAGACAGAGATGCAACAGATATGTCTATATACAACTGATACACA 1412
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Db 1320 CCAGCATGATCTGTGCGGCTTCTGTACAGGGGAAGCTGATTTCTTCCAGGGGTGACAGT 1379

Qy 1473 GAGGGCTCTGTGTCATCTTGAAGAACAAATATCTGTGTAGGGGATACAAAGCTGG 1532
Db 1380 GAGGGCTCTGTGTCATCTTGAAGAACAAATATCTGTGTAGGGGATACAAAGCTGG 1439
Qy 1533 GGTTCGTGCTGTCCAAAGCTTACAGACAGAGGTGTAGGGGAATGTATTCACG 1592
Db 1440 GGTTCGTGCTGTCCAAAGCTTACAGACAGAGGTGTAGGGGAATGTATTCACG 1499
Qy 1593 GACTGATTTATGACAAATAGAGGAGAGAGGCTTAATCCAGATGCTTGTCTTGAGC 1652
Db 1500 GACTGATTTATGACAAATAGAGGAGAGAGGCTTAATCCAGATGCTTGTCTTGAGC 1559
Qy 1653 TCGTTTACAAAGAAACAAATGGGGCTGTGTTTTCCTTCCCGTCAGATTTACTTTAGA 1712
Db 1560 TCGTTTACAAAGAAACAAATGGGGCTGTGTTTTCCTTCCCGTCAGATTTACTTTAGA 1619
Qy 1713 GATGATTCAGAGGTCACTTCTATTTATTAACAGTAAGTGTGTGGCTTGGCACTCT 1772
Db 1620 GATGATTCAGAGGTCACTTCTATTTATTAACAGTAAGTGTGTGGCTTGGCACTCT 1679
Qy 1773 CTGCAATTTCTGTGAGGCTGAGTGGCTCCCGCAGCTGCTCTCCCTAACCCCTTG 1832
Db 1680 CTGCAATTTCTGTGAGGCTGAGTGGCTCCCGCAGCTGCTCTCCCTAACCCCTTG 1739
Qy 1833 TCCGCAAGGGGTGATGGCGGCTGTGTGGGCACTGGCGTCAAGTGTGA--GGAGAG 1890
Db 1740 TCCGCAAGGGGTGATGGCGGCTGTGTGGGCACTGGCGTCAAGTGTGAAGGAAG 1799
Qy 1891 GGGTGAAGGCTG--CCCATTTAGATCTTCTGTGATGCTCTTTCAGGGGCAATTTTG 1949
Db 1800 GGGTGAAGGCTGCCCCCATTTAGATCTTCTGTGATGCTCTTTCAGGGGCAATTTTG 1859
Qy 1950 ATGAGCATGAGCTGTACACTCTCAGCTGTGATGATGATGAAAGGAAGAGACA 2009
Db 1860 ATGAGCATGAGCTGTACACTCTCAGCTGTGATGATGATGAAAGGAAGAGACA 1919
Qy 2010 TGAAGAGGAGACAGCCAGTGGCACCTGCAAGCGGCTG--CCTGTGGGGCCACTTGTGAT 2068
Db 1920 TGAAGAGGAGACAGCCAGTGGCACCTGCAAGCGGCTGCCCCGTGGGGCCACTTGTGAT 1979
Qy 2069 GTCCCAAGCTTACTCTCCCAAGGGGATTTTCTGTATGGGTTCTTATAGACTTACAGC 2128
Db 1980 GTCCCAAGCTTACTCTCCCAAGGGGATTTTCTGTATGGGTTCTTATAGACTTACAGC 2036
Qy 2129 CTGGAATGTTGGGCGCAGAAATTAAGGGACAGCCCTCATGGGTGGAGCTGTGATGAC 2188
Db 2037 CTGGAATGTTGGGCGCAGAAATTAAGGGACAGCCCTCATGGGTGGAGCTGTGATGAC 2095
Qy 2189 CTGTGAAGGGGACAGAAACATTTTGTCTTATGGGGTGAATATAGACATGGCCTT 2248
Db 2096 CTGTGAAGGGGACAGAAACATTTTGTCTTATGGGGTGAATATAGACATGGCCTT 2155
Qy 2249 GGGTGAAGGGGACAGAAATTAAGGGACAGCTTCCCTGTAGCACTCTGTGCTCAGTCTCA 2308
Db 2156 --GGTGAAGGGGACAGAAATTAAGGGACAGCTTCCCTGTAGCACTCTGTGCTCAGTCTCA 2214
Qy 2309 CTGCAATTTGGGTGGGGCTCTGTGGAGGGAGACTAGCTTCTCTCTCATCTCCCTGA 2368
Db 2215 CTGCAATTTGGGTGGGGCTCTGTGGAGGGAGACTAGCTTCTCTCTCATCTCCCTGA 2274
Qy 2369 CCCTGTCTTACAGCCCTGTGAGAGTGCATGCCCCCTTGTGCTGTGGGAGGGCGCCAG 2428
Db 2275 CCCTGTCTTACAGCCCTGTGAGAGTGT--ATGTCCCTTGTGCTGTGGAG--GGCGGCAAG 2331
Qy 2429 TCTGGACACATGTTGGCTTTCAGGCTGTCTGTACTGTGGAATGTAGGTCCATGGGG 2488
Db 2332 TTTGGACACATGCTGGCTTTCAGGCTGTGTATGTATGGAATGTAGGTCCATGGGG 2391
Qy 2489 AAATCAAGGATGCTCAGTTTAAGGTACAGTGTTCATGTTATGTTTCTACACATTTGCT 2547
Db 2392 AAATCAAGGATGCTCAGTTTAAGGTACAGTGTTCATGTTATGTTTCTACACATTTGCT 2450

RESULT 14
US-10-012-896-930
Sequence 930, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Kaloos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurell, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantabe, Yoshihito
APPLICANT: Meagher, Madeline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT FILING DATE: US/10/012.896
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 930
LENGTH: 1479
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-930
Query Match 42.5%, Score 1464.8; DB 9; Length 1479;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1477; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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DB 1 ATGGCTTGACTGAGGCTACCCAGCAGTATGAGCTTACTATGAAACCATGATAC 60
OY 209 CAACCGGAAACCCCTATCCGACAGCCCACTGTGTCCCACTGTCTAGAGGTGAT 268
DB 61 CAACCGGAAACCCCTATCCGACAGCCCACTGTGTGTCCCACTGTCTAGAGGTGAT 120
OY 269 CCGGCTGACTACTCCGTCCCGGTGCCAGTACGCCCGGAGGCTCTGACGAGCT 328
DB 121 CCGGCTGACTACTCCGTCCCGGTGCCAGTACGCCCGGAGGCTCTGACGAGCT 180
OY 329 TCCACCCCGTGTGTGACGAGCCCAATCCCATCCGGAGACGTGTGACCTCAAG 388
DB 181 TCCACCCCGTGTGTGACGAGCCCAATCCCATCCGGAGACGTGTGACCTCAAG 240
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DB 241 ACTAAGAAAGCACTGTGATCACTTGAACCCCTGAGGAGACTTCTGTGGAGACTCCGCTG 300
OY 449 GCCGCTGCTACTGTGAAGTTCAATGGGACAAAGTCTCCACTGTGGATAGAGTGC 508
DB 301 GCCGCTGCTACTGTGAAGTTCAATGGGACAAAGTCTCCACTGTGGATAGAGTGC 360
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DB 1440 GACTCTTAGTACTGATCAACCCCTTAAGTGTGTGATGGGTGTGACACTGCCCC 568

DB 361 GACTCTTAGTACTGATCAACCCCTTAAGTGTGTGATGGGTGTGACACTGCCCC 420
OY 569 GCGGGGAGGAGAGAAATCGGTGTGTGCGCTCTACGAGCAAACTTCCTTCAGGTG 628
DB 421 GCGGGGAGGAGAGAAATCGGTGTGTGTGCGCTCTACGAGATCAAACTTCCTTCAGGTG 480
OY 629 TACTCATCTCAGAGGAGTCTGTGSCACCCCTGTGTGCCAAGAGACTGGAACAGATAC 688
DB 481 TACTCATCTCAGAGGAGTCTGTGSCACCCCTGTGTGCCAAGAGACTGGAACAGATAC 540
OY 689 GGGGGGGGGCCCTGACAGGAGACATGGGCTATAGAAATATTTTACTGTAGCAAGAAATA 748
DB 541 GGGGGGGGGCCCTGACAGGAGACATGGGCTATAGAAATATTTTACTGTAGCAAGAAATA 600
OY 749 GTGATGACAGCGGATCCACAGCTTTATGAACAGCAAGTCCCGGCAATGTGCAT 808
DB 601 GTGATGACAGCGGATCCACAGCTTTATGAACAGCAAGTCCCGGCAATGTGCAT 660
OY 809 ATCTATATATATATCTGTACACAGTATGCTGTCTTCAAAAAGAGTGTCTTTACGC 868
DB 661 ATCTATATATATATCTGTACACAGTATGCTGTCTTCAAAAAGAGTGTCTTTACGC 720
OY 869 TGTATAGCTCTGGGGGTCACTTGAACCTCAAGCCCAAGAGAGATGTGGCGGCGAG 928
DB 721 TGTATAGCTCTGGGGGTCACTTGAACCTCAAGCCCAAGAGATGTGGCGGCGAG 780
OY 929 AGCGGCTCCCGGGGCGCTTGCGGCGAGTACGCTGACGCTCAAGAGCTCCACGT 988
DB 781 AGCGGCTCCCGGGGCGCTTGCGGCGAGTACGCTGACGCTCAAGAGCTCCACGT 839
OY 989 GTGCGAGGCTCATCATCACCCCGAGTGTGATGTGACAGCCCGCCACTCGGTGAAA 1048
DB 840 GTGCGAGGCTCATCATCACCCCGAGTGTGATGTGACAGCCCGCCACTCGGTGAAA 899
OY 1049 ACCCTTAAACAATCATGAGCATGAGCAGCATTCGCGGAGATTTTGAACATCTTTAT 1108
DB 900 ACCCTTAAACAATCATGAGCATGAGCAGCATTCGCGGAGATTTTGAACATCTTTAT 959
OY 1109 GTTCTATGAGCGGAGTACCAAGTGAAGAAAGTATTTCTATCCAAATTTATGATCCAA 1168
DB 960 GTTCTATGAGCGGAGTACCAAGTGAAGAAAGTATTTCTATCCAAATTTATGATCCAA 1019
OY 1169 GACCAAGAAACAATGATGAGCTGTGATGAGCTGACAGAGCTCTGACTTCAAGACCT 1228
DB 1020 GACCAAGAAACAATGATGAGCTGTGATGAGCTGACAGAGCTCTGACTTCAAGACCT 1079
OY 1229 AGTGAACAGGTGTGTGCCCAACCCAGGAGTATGTGTGACCCAGCAAGCTCTGCTG 1288
DB 1080 AGTGAACAGGTGTGTGTGCCCAACCCAGGAGTATGTGTGACCCAGCAAGCTCTGCTG 1139
OY 1289 GATTTCCGGGTGGGGGCGCACCGAGAGAAAGGAAAGCTCAGAAAGTGTGAACGCTGC 1348
DB 1140 GATTTCCGGGTGGGGGCGCACCGAGAGAAAGGAAAGCTCAGAAAGTGTGAACGCTGC 1199
OY 1349 CAAGGTCTTCTCATTTGAGACACAGAGATGCAACAGCATATGTCTATGACAACTGAT 1408
DB 1200 CAAGGTCTTCTCATTTGAGACACAGAGATGCAACAGCATATGTCTATGACAACTGAT 1259
OY 1409 CACACACAGCATGATCTGTGCCGCTTCTGACAGGGAACCTGATTTCTCCAGAGTGA 1468
DB 1260 CACACACAGCATGATCTGTGCCGCTTCTGACAGGGAACCTGATTTCTCCAGAGTGA 1319
OY 1469 CAGTGAAGGCGCTGTGTGACATTCGAAAGAAATTTGTGTGGCTGATAGGGGATACAG 1528
DB 1320 CAGTGAAGGCGCTGTGTGACATTCGAAAGAAATTTGTGTGGCTGATAGGGGATACAG 1379
OY 1529 CTGGGCTTCTGGCTGTGCCAAAGCTTTACAGACAGAGATGTACGGGAATGTATGATTT 1588
DB 1380 CTGGGCTTCTGGCTGTGCCAAAGCTTTACAGACAGAGATGTACGGGAATGTATGATTT 1439
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DB 1440 CACGAGCTGATTTATGACAAATGAGGCGACAGCGCTAA 1479


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RESULT 15
; US-09-895-793-930
; Sequence 930, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kaios, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 930
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-793-930

Query Match      42.5%; Score 1464.8; DB 9; Length 1479;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1477; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 149 AAGGCTTGAACACAGGAGGACACAGCAGCTATGGACCTTACTATGAAAAACATGATAC 208
DB 1 ATGGCTTTGAACACAGGAGGACACAGCAGCTATGGACCTTACTATGAAAAACATGATAC 60
QY 209 CAACCGGAAAAACCCATATCCCGACAGCCACAGCTGTGTCGCCCACTGTCTACGAGTGATC 268
DB 61 CAACCGGAAAAACCCATATCCCGACAGCCACAGCTGTGTCGCCCACTGTCTACGAGTGATC 120
QY 269 CCGGCTCAGTACTACCCGTCGCCCGTCCCGTCCAGTACGCCCCGAGGGTCTTGACGAGGCT 328
DB 121 CCGGCTCAGTACTACCCGTCGCCCGTCCCGTCCAGTACGCCCCGAGGGTCTTGACGAGGCT 180
QY 329 TCCAAACCCGCTGTCTGACAGCGACGCCCAATCCCATCCGGGACATGTGTCCACTCAAG 388
DB 181 TCCAAACCCGCTGTCTGACAGCGACGCCCAATCCCATCCGGGACATGTGTCCACTCAAG 240
QY 389 ACTAAGAAAGCACTGTGCATCATCTGACCCCTGGGAGACCTTCTCTGGAGGCTGGCGTG 448
DB 241 ACTAAGAAAGCACTGTGCATCATCTGACCCCTGGGAGACCTTCTCTGGAGGCTGGCGTG 300
QY 449 GCCGCTGCGCTACTGTGAAGATTTCATAGGACAGCAAGTGTCTCAACTCTGTGGATAGATGC 508
DB 301 GCCGCTGCGCTACTGTGAAGATTTCATAGGACAGCAAGTGTCTCAACTCTGTGGATAGATGC 360
QY 509 GACTCCTCAGGTACGTGCATCAACCCCTCTCACTGTGTGATGGCGTGTACACTGCCCC 568
DB 361 GACTCCTCAGGTACGTGCATCAACCCCTCTCACTGTGTGATGGCGTGTACACTGCCCC 420
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QY 569 GGGGGGAGGACGAAATCGGTGTGTCTGACGACCAACTTCATCTTCAAGTG 628
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QY 629 TACTCATCTCAGAGAAAGTCTGTGACCTGTGTGCCAGAGACATGGAAGATAC 688
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QY 809 ATCTATAAAAAACTGTACACAGTGAATCCCTGTCTTCAAAAGCAAGTGTCTTTACGC 868
DB 661 ATCTATAAAAAACTGTACACAGTGAATCCCTGTCTTCAAAAGCAAGTGTCTTTACGC 720
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DB 721 TGTATAGCCTGGGGGCAACTGAACCTCAAGCCGACAGACAGATCTGGGCGGAG 780
QY 929 AGCGCGCTCCCGGGGCGCTGGCCCTGGGACAGTCCAGCTCAGAGATGTGGCGGAG 988
DB 781 AGCGCGCTCCCGGGGCGCTGGCCCTGGGACAGTCCAGCTCAGAGATGTGGCGGAG 839
QY 989 GTGCGGAGGCTCCATCATACACCCCGAGTGATGTACACGCCGCCCATGTGTAAGAA 1048
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DB 960 GTTCTATGAGCCGGATATACCAAGTAGAAAAAGTATTTCTCATCAATATGACTCCAA 1019
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DB 1020 GACCAAGAACATGACATTCGCTGATGAAGTGTGACAGACCTGTGATCAACGACT 1079
QY 1229 AGTGAACCAAGTGTGTGTCGCCAACCCAGGACATGATGTCTGACCAAGACGCTGCTG 1288
DB 1080 AGTGAACCAAGTGTGTGTCGCCAACCCAGGACATGATGTCTGACCAAGACGCTGCTG 1139
QY 1289 GATTTCCGGGTGGGGGCGCCAGAGGAAAGGAAAGACCTCAGAAGTGTGAAGCGTGC 1348
DB 1140 GATTTCCGGGTGGGGGCGCCAGAGGAAAGGAAAGACCTCAGAAGTGTGAAGCGTGC 1199
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DB 1200 CAAGGTGCTTCTCATTTGAGACACAGAGATGCAACAGCATATGTCTATGACAACTGAT 1259
QY 1409 CACACCAGCCATATCTGTGTCCCGCTTCTGACAGGGGAAAGTGTGATTTCTGCCAGGTGA 1468
DB 1260 CACACCAGCCATATCTGTGTCCCGCTTCTGACAGGGGAAAGTGTGATTTCTGCCAGGTGA 1319
QY 1469 CAGTGGAGGCTCTGTGTCACCTTCGAAGAACATATCTGTGCTGTATAGGGATCAAG 1528
DB 1320 CAGTGGAGGCTCTGTGTCACCTTCGAAGAACATATCTGTGCTGTATAGGGATCAAG 1379
QY 1529 CTGGGGTTCGTGCTGTGCCAAAGCTTACAGACAGAGTGTACGGGAATGTGATGTATT 1588
DB 1380 CTGGGGTTCGTGCTGTGCCAAAGCTTACAGACAGAGTGTACGGGAATGTGATGTATT 1439
QY 1589 CACGCACTGGATTTATTCGAACAAATGAGGGCAGACGGCTAA 1628
DB 1440 CACGCACTGGATTTATTCGAACAAATGAGGGCAGACGGCTAA 1479
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Thu Jan 16 09:33:07 2003

us-09-807-201-8.rnpb

Page 24

Search completed: January 16, 2003, 08:32:07
Job time : 1021 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 08:39:45 ; Search time 44814 Seconds

(without alignments)
2235.930 Million cell updates/sec

Title: US-09-807-201-8

Perfect score: 3443
Sequence: 1 gggcgggcgggcgagtag.....ctgttcacatggcgtagata 3443Scoring table: IDENTITY_MDC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2:  gb_hg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_vl:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pin:*
35: em_hg_rod:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sy:*
39: em_hgo_hum:*
40: em_hgo_mus:*
41: em_hgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336.6	94.0	3966	6 AX041973	AX041973 Sequence
2	3136.8	91.1	3245	6 AX201156	AX201156 Sequence
3	3136.8	91.1	3245	6 AX267955	AX267955 Sequence
4	3127.2	90.8	3226	6 AF329454	AF329454 Homo sapi
5	2309.4	67.1	2479	6 AX201121	AX201121 Sequence
6	2309.4	67.1	2479	6 AX207965	AX207965 Sequence
7	2309.4	67.1	2479	6 AX267920	AX267920 Sequence
8	2309.4	67.1	2479	6 AX306771	AX306771 Sequence
9	2309.4	67.1	2479	6 AX395318	AX395318 Sequence
10	2309.4	67.1	2479	9 HSU75329	U75329 Human serin
11	1769.4	51.4	60904	9 AC005612	AC005612 Homo sapi
12	1767.8	51.3	43003	9 HS87D5	AL773571 Homo sapi
13	1763	51.3	313064	9 HSMX1B	AL442167 Homo sapi
14	1763	51.2	108927	9 AP001609	AP001609 Homo sapi
15	1763	51.2	132110	9 AP001610	AP001610 Homo sapi
16	1763	51.2	340000	9 HS21C085	AL161285 Homo sapi
17	1712.4	49.7	1740	9 AF270487	AF270487 Homo sapi
18	1710.4	49.7	1738	6 AX395316	AX395316 Sequence
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ALIGNMENTS

RESULT 1	AX041973	3966 bp	DNA	linear	PAT 23-NOV-2000
LOCUS	AX041973				
DEFINITION	Sequence 3 from Patent WO0065067.				
ACCESSION	AX041973				
VERSION	AX041973.1	GI:11340738			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 3966)				
	Nelson, P.S., Hood, L., and Lin, B.				
	Prostate-specific polynucleotides, polypeptides and their methods				
	of use				

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 AX201156
 VERSION AX201156.1 GI:15390911
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3245)
 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
 Compositions and methods for the therapy and diagnosis of prostate cancer
 Patent: WO 0151633-A 786 19-JUL-2001; CORIXA CORPORATION (US)

JOURNAL
 FEATURES
 source location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 ORIGIN

Query Match 91.1%; Score 3136.8; DB 6; Length 3245;
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1/29/03

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ACCESSION	AF329454		
VERSION	AF329454.1	GI:14091027	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Jacquinet, E., Rao, N.V., Rao, G.V., Zhengming, W., Albertine, K.H. and Holzel, J.R.		
TITLE	Cloning and characterization of the cDNA and gene for human epitheliasin		
JOURNAL	Eur. J. Biochem. 268 (9), 2687-2699 (2001)		
MEDLINE	21223025		
PUBMED	11322890		
REFERENCE	2 (bases 1 to 3226)		
ADTHORS	Jacquinet, E., Rao, N.V., Rao, G.V., Wang, Z., Albertine, K.H. and Holzel, J.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-DEC-2000) Pulmonary Medicine, University of Utah, 50N. Medical Dr., Salt Lake City, UT 84132, USA		
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Best Local Similarity	99.6%; Pred. No. 0;		
Matches 3188; Conservative	0; Mismatches 8; Indels 6; Gaps 5;		

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RESULT 5
AX201121

LOCUS AX201121 2479 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 751 from Patent WO0151633.
ACCESSION AX201121
VERSION AX201121.1 GI:15390895
KEYWORDS
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ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2479)
REFERENCE Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
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JOURNAL Patent: WO 0151633-A 751 19-JUL-2001;
CORIXA CORPORATION (US)
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DEFINITION	Sequence 69 from Patent WO0157194.		
ACCESSION	AX207965		
VERSION	AX207965.1	GI:15422561	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Madison, E.L., Ong, E.O. and Yeh, J.C.		
TITLE	Nucleic acid molecules encoding transmembrane serine proteases, the encoded proteins and methods based thereon		
JOURNAL	Patent: WO 0157194-A 69 09-AUG-2001; CORVAS INTERNATIONAL, INC. (US)		
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VERSION
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SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
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AUTHORS
Ku,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL
Patent: WO 0173032-A 894 04-OCT-2001;
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Matches 2425; Conservative 0; Mismatches 21; Indels 13; Gaps 9;
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REFERENCE
AUTHORS Macbeth,K.J. and Shyjan,A.W.
TITLE Expression analysis of specific nucleic acids and polypeptides
JOURNAL useful in the diagnosis and treatment of prostate cancer
Millennium Pharmaceuticals, Inc. (US)
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ACCESSION AX395318
VERSION AX395318.1 GI:21066314
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Saferran,D., Raitano,A.B., Hubert,R.S., Jakobovits,A., Paris,M. and
Challita-Eld,P.M.
TITLE Novel tumor antigen useful in diagnosis and therapy of bladder,
ovary, lung and kidney cancers
JOURNAL Patent: WO 0204953-A 3 17-JAN-2002;
Agensis, Inc. (US)
FEATURES
source Location/Qualifiers
1..2479
BASE COUNT 578 a 650 c 677 g 574 t
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VERSION	U75329.1		
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2479) Padoloni, Giacobino, A., Chen, H., Peltsch, M.C., Rossier, C. and Antonarakis, S.E.		
TITLE	Cloning of the TMPRSS2 gene, which encodes a novel serine protease with transmembrane, LDIARA, and SRCR domains and maps to 21q22.3		
JOURNAL	Genomics 44 (3), 309-320 (1997)		
MEDLINE	97468144		
PUBMED	9325052		
REFERENCE	2 (bases 1 to 2479)		
AUTHORS	Padoloni, Giacobino, A., Chen, H. and Antonarakis, S.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-OCT-1996) Medical Genetics, University of Geneva Medical School, 1 Michel-Servet Street, Geneva 1211, Switzerland		
FEATURES	Location/Qualifiers		

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DEFINITION sequence.
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VERSION AC005612.1 GI:3540153
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 60904)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miquel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE Sequencing of human chromosome 21
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 60904)
AUTHORS Rhee,P.O.
TITLE Large Scale Sequence Analysis and Annotation with the Sequence
JOURNAL Comparison Analysis (SCAN) System
REFERENCE 3 (bases 1 to 60904)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Davis,C.A., Kadner,K., Miquel,T., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE Direct Submission

JOURNAL Submitted (04-SEP-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
COMMENT Sequence submitted by:
DOE Joint Genome Institute.
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 AC AL442167; A011929;
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 SV AL442167.1
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 DT 23-SEP-2000 (Rel. 65, Last updated, Version 1)
 XX
 DE Homo sapiens chromosome 21 from 5 PACs and 5 Cosmids map
 DE 21q22.2;D21S349-MX1; segment 2/2
 XX
 KW HTG.
 KW
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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 RA Ramser J., Francis F., Beck A., Hennig S., Klages S., Borzym K., Langer I.,
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 RP
 RL Unpublished.
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DEFINITION	Homo sapiens genomic DNA, chromosome 21, clone: KB447A5, MX1-D21S171		
ACCESSION	AP001609		
VERSION	AP001609.1		
KEYWORDS	HTG.		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 108927)		
TITLE	Shimizu,N., Kudoh,J. and Shibuya,K.		
FEATURES	Homo sapiens genomic DNA, chromosome 21, clone: KB447A5, MX1-D21S171 region		
JOURNAL	Published Only in Database (2000)		
REFERENCE	2 (bases 1 to 108927)		
AUTHORS	Shimizu,N., Kudoh,J. and Shibuya,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-APR-2000) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku ku, Tokyo 160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)		
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DEFINITION MX1-D21S171 region, complete sequence.
ACCESSION AP001610
VERSION AP001610.1 GI:7670564
KEYWORDS HUG:
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REFERENCE 1 (bases 1 to 132110)
AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
TITLE Homo sapiens genomic DNA, chromosome 21, clone:ClT2533B8,
MX1-D21S171 region
Published Only in Database (2000)
2 (bases 1 to 132110)
JOURNAL Shimizu,N., Kudoh,J. and Shibuya,K.
REFERENCE Direct Submission
AUTHORS Nobuyoshi Shimizu, Kyo University, School
TITLE Submitted (04-Apr-2000) Nobuyoshi Shimizu, Kyo University, School
JOURNAL of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
FEATURES Location/Qualifiers

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